

02 4/16

CR7

Access DB# 91485

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: K. Cochrane Carlson Examiner #: 70146 Date: 4-8-03
 Art Unit: 1653 Phone Number: 308 0034 Serial Number: 09709585
 Mail Box and Bldg/Room Location: 9301 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search and interference
 search Seq ID NO:2, also 15 consecutive
 aa of Seq ID NO:2.

This is a reissue application. The
 CR7 is in SN 08/401530

POINT OF CONTACT:
 PAUL SCHULWITZ
 TECHNICAL INFO. SPECIALIST
 GM1 0000 TEL. (703) 305-1954

Thanks
 Karen

4-14

- Mark Spencer says to search the patent 5,834,590
 see attached

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>4/16</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>4/16</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>5</u>	Other _____	Other (specify) _____

Carlson, Karen

From: Spencer, Mark
Sent: Monday, April 14, 2003 10:36 AM
To: Carlson, Karen
Subject: RE: 09/709585 is a re-issue of 08/401530

Karen,

The sequences for 08/401,530 can be searched in the issued database under patent number 5834590. I checked the database and the sequences are there. Let Mary Hale and I know if you have any further trouble.

Thanks,
Mark

-----Original Message-----

From: Carlson, Karen
Sent: Monday, April 14, 2003 8:06 AM
T : Spencer, Mark
Subject: 09/709585 is a re-issue of 08/401530

Hi Mark,

I need to re-search a sequence in '530 for a reissue application. Leonard in STIC says that '530 does not have a CRF and the sequences are in a public database and not searchable by STIC from that venue.

Can this be corrected?

Thanks!

Karen Cochrane Carlson

AU 1653

CM1 10A07

Mailbox CM1 9B01

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: April 16, 2003, 10:40:45 ; Search time 36 Seconds

(without alignments)
644.045 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MPMPTLCRMGMMLISCLMFL.....QKWRDFCNELPYCKFRV 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq.101002:*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958	100.0	174	AA98525	Hamster islet neog
2	958	100.0	175	AA64790	INGAP protein frag
3	605.5	63.2	175	AA54097	Mus PAP. Mus mu
4	593	61.9	175	AA95089	Reg-2 protein. Ra
5	593	61.9	175	AA18614	Amino acid sequenc
6	572	59.7	175	AA54098	Mouse PAP. Mus mu
7	572	59.7	175	AA57117	Human Pancreatitis
8	572	59.7	183	AA54568	Human Cancer assoc
9	566	59.1	174	AA14795	Fragment A3 from h
10	557	58.1	175	AAW1682	Human pancreatitis

11	557	58.1	175	20	AA41755	Human PRO162 prote
12	557	58.1	175	21	AA44311	Human PRO162 (UNO4
13	557	58.1	175	22	AAU29235	Human PRO polypept
14	557	58.1	175	23	AB95482	Human angiotensin
15	557	58.1	175	23	AB84876	Human PRO162 prote
16	557	58.1	175	12	AA14797	Rat pancreatitis a
17	525.5	54.9	175	11	AA05904	Bovine pancreatic
18	522	54.5	210	22	ABG18688	Novel human diago
19	484	50.5	158	12	AA14796	Fragment A2 from r
20	408.5	42.6	174	21	AA54301	Human pancreatit
21	395.5	41.3	165	9	AA81513	Sequence encoded b
22	395.5	41.3	165	9	AA81518	Sequence encoded b
23	395.5	41.3	165	15	AA85928	Rat reg protein.
24	394.5	41.2	165	10	AA94615	Rat reg protein.
25	387	40.4	121	22	ABG18687	Novel human diago
26	386.5	40.3	165	14	AA84535	MUREG-1. Mus musc
27	386.5	40.3	174	21	AA843737	Human cancer assoc
28	386	40.3	173	14	AA84536	MUREG-2. Mus musc
29	385.5	40.2	166	15	AA85928	Human reg protein.
30	385.5	40.2	166	22	AA81653	Human colon associ
31	385.5	40.2	166	22	AA81656	Human reg protein
32	379.5	39.6	166	10	AA94614	Human reg protein.
33	378.5	39.5	166	9	AA81514	Sequence encoded b
34	362.5	37.8	146	15	AA86594	Rat reg protein (G
35	354.5	37.0	144	15	AA86595	Rat reg protein (G
36	342.5	35.8	147	11	AA806425	Human reg protein
37	341.5	35.6	146	15	AA86591	Human reg protein
38	333.5	34.8	144	15	AA86592	Human reg protein
39	323.5	33.8	133	15	AA86596	Rat reg protein (I
40	303.5	31.7	133	15	AA86593	Human reg protein
41	257.5	26.9	294	22	ABG01855	Novel human diago
42	257.5	26.9	406	22	ABG03060	Novel human diago
43	257.5	26.9	558	22	ABG00465	Novel human diago
44	250	26.1	106	21	AA844108	Human cancer assoc
45	209.5	21.9	240	22	ABG20353	Novel human diago

ALIGNMENTS

RESULT 1	AA98525	standard; Protein, 174 AA.
AA98525	AA98525	
AC	AA98525	
DT	18-APR-1997	(first entry)
XX		
DE	Hamster islet neogenesis associated protein.	
XX		
KW	Hamster islet neogenesis associated protein; INGAP; pancreas; endocrine;	
KW	proliferation; pancreatic tissue; celiothane; duct epithelium; homology;	
KW	differential display method; open reading frame; liver; adenocarcinoma;	
KW	pancreatitis associated protein; lithostatine; pancreatic stone protein;	
KW	beta-cell; regeneration; insulin; diabetes; mammal.	
XX		
OS	Cricetulus sp.	
XX		
PN	WO9626215-A1.	
PD	29-AUG-1996.	
XX		
PF	12-FEB-1996;	96WO-US01528.
XX		
PR	07-NOV-1995;	95US-0006271.
PR	22-FEB-1995;	95US-0401530.
XX		
PA	(EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.	
XX		
PI	Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L;	
PI	Vinik AJ;	
XX		
XX	WPI, 1996-402318/40.	

DR N-PSDB; AAT36612.
 XX Mammalian islet neo:genesis associated protein - isolated by
 PT stimulating mammalian pancreas by wrapping in cellopahane, for
 PT treatment of diabetes, etc
 XX-
 PS Claim 2; Page 26; 50pp; English.
 CC This is the amino acid sequence of the hamster islet neogenesis
 CC associated protein (INGAP). The gene is isolated from pancreatic cells
 CC which are induced to proliferate upon wrapping pancreatic tissue in
 CC cellopahane. Wrapping of the pancreas stimulate proliferation of new
 CC endocrine cells which appear from duct epithelium. The INGAP gene was
 CC isolated from a cDNA library constructed from mRNA purified from
 CC cellopahane wrapped hamster pancreas using a differential display method
 CC to compare genes expressed in cellopahane-wrapped and control pancreas
 CC The gene contains an open reading frame which encodes a protein of 175
 CC amino acids. The protein has structural homology to the pancreatic
 CC associated protein (PAP)/HIP family of genes which is associated with
 CC pancreatic or liver adenocarcinoma, and to the Reg/PSP/lithostatine
 CC (PSP = pancreatic stone protein) family of gene which has been shown to
 CC stimulate pancreatic beta cell growth and may be involved in pancreatic
 CC islet regeneration. The protein can be used to stimulate islet cell
 CC proliferation in (non-)insulin dependent diabetic mammals.
 CC
 SO Sequence 174 AA;
 Query Match 100.0%; Score 958; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 2.8e-88;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSAVAGSYCYSLILIPQW 60
 DB 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSAVAGSYCYSLILIPQW 60
 OY 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAQYIWIGLHDPHGTLPNGSGWK 120
 DB 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAQYIWIGLHDPHGTLPNGSGWK 120
 OY 121 WSSSNVLTFFYNNERNPSTADRGYCAVLSQKSGFQKWRDNCENELPYICKRFV 174
 DB 121 WSSSNVLTFFYNNERNPSTADRGYCAVLSQKSGFQKWRDNCENELPYICKRFV 174
 RESULT 2
 AAM64790
 ID AAM64790 standard; Protein; 175 AA.
 XX AAM64790;
 AC
 XX 18-NOV-1998 (first entry)
 DT
 XX
 DE INGAP protein fragment.
 XX
 KW INGAP; islet neogenesis-associated protein; treatment; diabetes;
 KW host cell.
 XX
 OS Unknown.
 OS
 PN US5804421-A.
 PD 08-SEP-1998.
 XX
 PF 12-AUG-1997; 97US-0909725.
 XX
 PR 12-AUG-1997; 97US-0909725.
 PR 30-OCT-1996; 96US-0741096.
 XX
 PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
 XX Barlow SM, Piltenger GL, Rafaeloff-Phail R, Vink AI;
 PI WPI; 1998-505656/43.
 DR

XX Expression of islet neogenesis-associated protein - from recombinant
 PT construct lacking signal peptide, useful in the treatment of
 PT diabetes
 PT
 PS Claim 1; Column 19-20; 14pp; English.
 CC This sequence represents INGAP, an islet neogenesis-associated protein.
 CC This sequence is used in the construction of a recombinant construct
 CC having a coding sequence lacking a signal sequence and which is operably
 CC linked to transcription and translation initiation sites. This construct
 CC in a host cell is useful for producing recombinant mature INGAP, which
 CC is useful in the treatment of diabetes. High levels of INGAP expression
 CC can be achieved in bacterial and eukaryotic cells by removing the signal
 CC peptide as it is possibly toxic to cells.
 CC
 SO Sequence 175 AA;
 Query Match 100.0%; Score 958; DB 19; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.8e-88;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSAVAGSYCYSLILIPQW 60
 DB 2 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSAVAGSYCYSLILIPQW 61
 OY 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAQYIWIGLHDPHGTLPNGSGWK 120
 DB 62 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAQYIWIGLHDPHGTLPNGSGWK 121
 OY 121 WSSSNVLTFFYNNERNPSTADRGYCAVLSQKSGFQKWRDNCENELPYICKRFV 174
 DB 122 WSSSNVLTFFYNNERNPSTADRGYCAVLSQKSGFQKWRDNCENELPYICKRFV 175
 RESULT 3
 AAR54097
 ID AAR54097 standard; Protein; 175 AA.
 XX AAR54097;
 AC
 XX 01-FEB-1995 (first entry)
 DT
 XX
 DE Mouse PAP.
 XX
 KW Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
 KW aggregation; antibacterial; primer; PCR.
 XX
 OS Mus musculus.
 OS
 PN JP06135998-A.
 PD 17-MAY-1994.
 XX
 PF 22-OCT-1992; 92JP-0284765.
 XX
 PR 22-OCT-1992; 92JP-0284765.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 DR WPI; 1994-197103/24.
 DR N-PSDB; AAO64171.
 XX
 PF Human and mouse pancreatitis-associated protein (PAP) - useful
 PT for prepn. of proteinaceous antibacterial agent
 PS
 PS Claim 1-6; Page 5-6; 7pp; Japanese.
 CC PAP DNA has a high bacteria-aggregating activity and is useful for
 CC the prepn. of PAP which can act as a proteinaceous antibacterial
 CC agent. Total RNA was isolated from mouse. It was hybridised with a
 CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
 CC Two primers are given in AAO64173-74.

XX	Sequence	175 AA:	Score	605.5:	DB:15:	Length	175:
SO	Query Match	63.2%:	Pred. No. 7.5e-53:				
	Best Local Similarity	60.7%:					
	Matches 105: Conservative	29:	Mismatches 30:				
QY	1	MLPMLCLR-MSWMLLSCTMLFSLWGEESQKLLPSSRTICPCPGSAVAGSYGSLILIPQT	59				
Db	1	MLPPLACSVMSWMLLSCTMLLSQYQGEESLKNIPARICSPKGSQAAYGSCYALPQIPQT	60				
QY	60	WSNAELSCOMHEHSGHLAFLSTGELTFPVSLVKNLSLTAAQYIWMIGHLHDSHTLPNGSGM	119				
Db	61	WDAELACQKRGGLHLYSLNLSAELSFSSMWKRRGNSQYIWMIGHLHPTLAEAPRNGGM	120				
QY	120	KWSSSNVLFTYWMERNPSTADRGYCAVLSQKSGFQKMRDENCENLPYICAF	172				
Db	121	EWSNDVNNYFWERNPSTALDRACGSLTASAGFLKWDMDTCCEKPLPYVCF	173				

ID	AAW95089		standard; Protein;	175 AA.
XX AC	AAW95089;			
XX DT	20-MAY-1999	(first entry)		
DE XX	Reg-2 protein.			
XX KW	Reg-2; Schwann cell mitogen; repair; regenerate; neuronal cell; tissue;			
KM RW	glial growth factor; neuroglin.			
OS XX	Rattus sp.			
PX PN	GB2329335-A.			
PD XX	24-MAR-1999.			
PF PE	16-SEP-1998;	98GB-0020193.		
PR XX	17-SEP-1997;	97GB-0019796.		
PA XX	(MED-) MEDICAL RES COUNCIL.			
PI PI	Hunt SP,	Livsey FJ;		
AX XX	WPI:	1999-156299/14.		
DR XX	N-PSTDB;	AAX26126.		
PT PT	Use of a protein (Reg-2) to manufacture a Schwann cell mitogen. - to			
PT PT	repair and/or regenerate neuronal cells or tissue, either in vivo,			
PT PT	or in vitro and then introduced into subject			
PS PS	Claim 1; Page 24; 33pp; English.			
CC CC	The invention relates to the use of a protein (Reg-2) or its variant,			
CC CC	derivative or homologue to manufacture a Schwann cell mitogen. Reg-2 is			
CC CC	used to repair and/or regenerate neuronal cells or tissue. Neuronal cells			
CC CC	or tissue may be repaired and/or regenerated either in vivo, or in vitro			
CC CC	and thus introduced into a subject. Reg-2 unlike known Schwann cell			
CC CC	mitogens e.g. glial growth factors/neurogelins, are upregulated during			
SC SC	regeneration. The present sequence represents the Reg-2 protein.			
SQ SQ	Sequence	175 AA;		
Query Match		61.9%; Score 593; DB 20; Length 175;		
BEST Local Similarity		61.0%; Pred. No. 1,3e-51;		
MATCHES 100; Conservative		30; Mismatches 34; Indels 0; Gaps 0		
OY	MSMMILSCIIMFTLSWGCESSOKRLPDSRTICPGGSVAVGYCTSLIIPOTWSNAELSCQ	68		
DH	: : : : :: :: : :: 10 MSMTLLSCLMLISQVOVGEDSPKRIIPSARKTSCPPGSGQAIGSYCYALFDIPTWTDAEIAQCQ	69		

[illegible]

ID	AAB18614 standard; Protein: 175 AA.
AC	AAB18614;
Dt	15-JAN-2001 (first entry)
DE	Amino acid sequence of a rat Reg-2 polypeptide.
KW	Schwann cell mitogen; Reg-2; neuronal cell regeneration; motor neuron; neuron-glia interaction.
OS	Rattus sp.
Pn	GB2347931-A.
pD	20-SEP-2000.
PF	02-FEB-2000; 2000GB-0002424.
PR	17-SEP-1997; 97GB-0019796. 16-SEP-1998; 98GB-0020193.
PA	(MEDIC-) MEDICAL RES COUNCIL.
PI	Livesey FJ, Hunt SP:
DR	WPLI; 2000-567204/53. N-PsDB; AAA75486.
PT	New Schwann cell mitogen (known as Reg-2), useful for repair and regeneration of neuronal cells and tissue, is upregulated during neuronal regeneration -
Px	Claim 2; Page 24; 32pp; English.
Cc	The present sequence represents a Schwann cell mitogen, known as Reg-2. Reg-2 can be upregulated during regeneration of neuronal cells and tissue. Reg-2 is an essential component in neuron-glial interaction that underlies development and regeneration of mammalian motor neurons. It is a 16 kDa protein. Reg-2 is used to affect development of neurons cells and tissue, especially for promoting their repair and regeneration, particularly of motor cells in adult humans.
sQ	Sequence 175 AA:
Query Match	61.9%; Score 593; DB 21; Length 175;
Best Local Similarity	61.0%; Pred. No. 1.3e-51;
Matches 100; Conservative	30; Mismatches 34; Indels 0; Gaps 0.
Oy	MSMWLLSCLMFWSWGSESOOKLPSSRTCPGSGVAAGSYCSLILIPOTMNAELSCO 68
Bd	S C ::: : : : : : : 10 MSWMILLSCMLLSOVGDSPKTIIPSARISCRPGSQATSTCYALPQTWPDALACO 69
Oy	MHFSGLIAFLLTGTETFWSLVYKNLSLAYOYTIGLIHDPSHGTLDPNGSGMKWSSNVLT 128
Bd	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: 70 KREGHIVSVLVNYEASFTLASMYKNTGNYSXYTWIGLIDPLETAGEBNGGWEMSNDDIMN 129
Oy	FYMWERNPSTAADRGCAVLISOXSKGRQRKDPCENBELPYCKE 172
Bd	: : : : : : : : : 130 FYMERPNPSTAIADRGCGLSRSSGFRLRMWDITCEVKLPVCYE 173

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RESULT 6
ID AAR54098 standard; Protein; 175 AA.
XX-
AC AAR54098;
DT 01-FEB-1995 (first entry)
DE Mouse PAP.
XX
KW Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
KW aggregation; antibacterial; primer; PCR.
XX
OS Mus musculus.
XX
PN JP06135998-A.
XX
PD 17-MAY-1994.
XX
PF 22-OCT-1992; 92JP-0284765.
XX
PR 22-OCT-1992; 92JP-0284765.
XX
PS (SHIO ) SHIONOGI & CO LTD.
XX
PA WPI; 1994-197103/24.
XX
DR N-PSDB; AA064172.
XX
PT Human and mouse pancreatitis-associated protein (PAP) - useful
PT for prepn. of proteinaceous antibacterial agent
XX
PS Claim 7-12; Page 6-7; 7pp; Japanese.
XX
CC PAP DNA has a high bacteria-aggregating activity and is useful for
CC the prepn. of PAP which can act as a proteinaceous antibacterial
CC agent. Total RNA was isolated from mouse. It was hybridised with a
CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
CC Two primers are given in AA064173-74.
XX
SQ Sequence 175 AA;

Query Match          59.7%; Score 572; DB 15; Length 175;
Best Local Similarity 57.6%; Pred. No. 1.7e-49;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

OY 3 PMTICRMSMMLSCIMFLSWVEGEESOKLPSSRITCPQGSVAYGSYCYSLILIPOTWSN 62
DB 4 PMALPSYSWMLSCIMFLSWVEGEESOKLPSSRITCPQGSVAYGSYCYSLILIPOTWSN 62
OY 63 AELSCOMHFSGHIAFLISTGEITTFVSSLVKNSLTAYQYIWMIGLHDPHSGTLPNGSGWKMS 122
DB 64 ADLACOKRPSGNLVSLGAEBSFVSLVKSIGNSYSYVMIGLHDPHSGTLPNGSGWKMS 123
OY 123 SSNVLTFFYMERNPSTIAADRGCAVLQSGFQKMRDNCENELPYCKF 172
DB 124 SSDVMNTFAWERNPSTISSPGHCASLSRSTAFLRKMDYNCNVRLLPYCKF 173

RESULT 7
ID AAR57117 standard; Protein; 175 AA.
XX
AC AAR57117;
DT 21-FEB-1995 (first entry)
DE Human Pancreatitis-Associated Protein.
XX
KW Human PAP; pancreatitis-associated protein; diagnosis; detection;
KW cystic fibrosis transmembrane conductance regulator; CFTR gene;
KW mucoviscidosis.
XX

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OS Homo sapiens.
XX
PN W09415218-A.
XX
PD 07-JUL-1994.
XX
PF 23-DEC-1993; 93WO-FR01299.
XX
PR 24-DEC-1992; 92FR-0015730.
XX
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI Dagorn J, Iovanna J, Keim V, Sarles J;
XX
DR WPI; 1994-234870/28.
XX
DR N-PSDB; AA069201.
XX
PT In vitro detection of pancreatic disease associated with CFTR
PT gene mutation - by measuring concn. of pancreatitis associated
PT protein in blood etc., suitable for neonatal diagnosis of, e.g.
PT cystic fibrosis
XX
PS Claim 1; Fig 3; 33pp; French.
XX
CC Antibodies which recognise the previously isolated and sequenced
CC human Pancreatitis-Associated protein (PAP) are claimed. They are
CC useful for measuring the amount of PAP in a sample to detect
CC pancreatic disease associated with heterozygotic mutations in the
CC CFTR gene. Such conditions result in expression of PAP at levels
CC at least 2-3 times higher than normal.
XX
SQ Sequence 175 AA;

Query Match          59.7%; Score 572; DB 15; Length 175;
Best Local Similarity 57.6%; Pred. No. 1.7e-49;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

OY 3 PMTICRMSMMLSCIMFLSWVEGEESOKLPSSRITCPQGSVAYGSYCYSLILIPOTWSN 62
DB 4 PMALPSYSWMLSCIMFLSWVEGEESOKLPSSRITCPQGSVAYGSYCYSLILIPOTWSN 62
OY 63 AELSCOMHFSGHIAFLISTGEITTFVSSLVKNSLTAYQYIWMIGLHDPHSGTLPNGSGWKMS 122
DB 64 ADLACOKRPSGNLVSLGAEBSFVSLVKSIGNSYSYVMIGLHDPHSGTLPNGSGWKMS 123
OY 123 SSNVLTFFYMERNPSTIAADRGCAVLQSGFQKMRDNCENELPYCKF 172
DB 124 SSDVMNTFAWERNPSTISSPGHCASLSRSTAFLRKMDYNCNVRLLPYCKF 173

RESULT 8
ID AAB43568 standard; Protein; 183 AA.
XX
AC AAB43568;
DT 08-FEB-2001 (first entry)
DE Human cancer associated protein sequence SEQ ID NO:1013.
XX
KW Human: cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnereary; immunomodulator;
KW antidiabetic; antiasclerotic; antirheumatic; antitumoral; antiviral;
KW antiinflammatory; antifibrotic; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; noctropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
OS Homo sapiens.
XX

```

PN WO2005350-A1.
 XX 21-SEP-2000.
 PD 08-MAR-2000; 2000WO-US05882.
 XX 12-MAR-1999; 99US-0124270.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 XX WPI: 2000-587533/55.
 DR N-PSDB; AAC77777.
 XX Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -
 PS Claim 11; Page 1593-1594; 2352pp; English.
 CC AAC7607 to AAC78448 encode the human cancer associated proteins given
 CC in ABA43398 to ABA44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antistimatic; antirheumatic; antitumor;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC rejection, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and ABA44240 represent sequences used in the exemplification of
 CC the present invention.
 XX Sequence 183 AA;
 SQ
 Query Match 59.7%; Score 572; DB 21; Length 183;
 Best Local Similarity 57.6%; Pred. No. 1.8e-49;
 Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

OY 3 PWTLCRMWMLSCIMFLSWVEGEESOKLPSSRTTCOGSVAYGSCYSLILIPQTMEN 62
 DB 12 PMLPSVSMWMLSCIMFLSWVOGEPEPRLPSARIRCPKSKAYGSHCYALFLSPKSWTD 71
 OY 63 AELSCOMHFSGLAFLSTGETTFVSSLVKNSLTAYOYIWIIGLHDPSSHGTLPNGSGWKMS 122
 DB 72 ADLACQKRPSGNLYSVLSGAGSFVSLVKSIGNSYWIWIGLHDPDTGTEPNNGSGWKMS 131
 OY 123 SSNVLTFTYNNWRNPSTIAADRGYCAVLSQSGFQKMRDNCENELPYICKF 172
 DB 132 SSDVMNYFAWERNPSTISPGHCASLSRSTAFLRKMDYNCNVRLPYCKF 181

RESULT 9
 AAR14795
 ID AAR14795 standard; Protein; 174 AA.
 AC AAR14795;
 XX 29-JAN-1992 (first entry)
 DE Fragment A3 from human pancreatitis associated protein.
 XX hPAP; pancreas; imaging; rat PSP.
 XX

OS Homo sapiens.
 XX WO9116428-A.
 XX 31-OCT-1991.
 PD 18-APR-1991; 91WO-FR00323.
 XX 20-APR-1990; 90FR-0005062.
 PR (INRM) INSERM INST NAT SANTE.
 PA Iovanna JL, Keim V, Dagron JC;
 XX WPI: 1991-339816/46.
 DR N-PSDB; AAQ14619, AAQ14623.
 XX CDNA fragment of human pancreatitis associated protein -
 PT produced by genetic engineering, and the corresponding antibody,
 PT for use in the diagnosis of pancreatitis
 PS Claim 13; Page 36; 49pp; French.
 CC The human PAP CDNA fragment S3 was cloned into pEX and the
 CC resultant recombinant transformed into E.coli. The expression
 CC product (A3) was used to generate antibodies for in vitro
 CC diagnosis of acute pancreatitis and for imaging the pancreas.
 XX Sequence 174 AA;
 SQ
 Query Match 59.1%; Score 566; DB 12; Length 174;
 Best Local Similarity 57.4%; Pred. No. 6.9e-49;
 Matches 97; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

OY 3 PWTLCRMWMLSCIMFLSWVEGEESOKLPSSRTTCOGSVAYGSCYSLILIPQTMEN 62
 DB 4 PMLPSVSMWMLSCIMFLSWVOGEPEPRLPSARIRCPKSKAYGSHCYALFLSPKSWTD 63
 OY 63 AELSCOMHFSGLAFLSTGETTFVSSLVKNSLTAYOYIWIIGLHDPSSHGTLPNGSGWKMS 122
 DB 64 ADLACQKRPSGNLYSVLSGAGSFVSLVKSIGNSYWIWIGLHDPDTGTEPNNGSGWKMS 123
 OY 123 SSNVLTFTYNNWRNPSTIAADRGYCAVLSQSGFQKMRDNCENELPYICKF 171
 DB 124 SSDVMNYFAWERNPSTISPGHCASLSRSTAFLRKMDYNCNVRLPYCKF 172

RESULT 10
 AAW71682
 ID AAW71682 standard; Protein; 175 AA.
 AC AAW71682;
 XX 04-DEC-1998 (first entry)
 DE Human pancreatitis-associated protein.
 XX Human pancreatitis-associated protein; PAP-2; agonist; pancreatitis;
 KW hyperplasia; hyperinsulinism; antagonist; tumour; oesophagus;
 KW intestine; metastases; Crohn's disease; ulcerative colitis;
 KW antibody; probe; PCR primer; amplification; hybridisation;
 KW inhibitor.
 XX Homo sapiens.
 OS WO9841633-A1.
 XX 24-SEP-1998.
 PD 20-MAR-1998; 98WO-US05699.
 XX 20-MAR-1997; 97US-0822261.
 XX

PR	11-MAR-1998	98US-0077651
PR	11-MAR-1998	98US-0077661
PR	11-MAR-1998	98US-0077669
PR	12-MAR-1998	98US-0077791
PR	13-MAR-1998	98US-0078004
PR	17-MAR-1998	98US-0040220
PR	20-MAR-1998	98US-0078886
PR	20-MAR-1998	98US-0078910
PR	20-MAR-1998	98US-0078936
PR	20-MAR-1998	98US-0078939
PR	25-MAR-1998	98US-0079294
PR	26-MAR-1998	98US-0079656
PR	27-MAR-1998	98US-0079663
PR	27-MAR-1998	98US-0079664
PR	27-MAR-1998	98US-0079689
PR	27-MAR-1998	98US-0079728
PR	30-MAR-1998	98US-0079786
PR	30-MAR-1998	98US-0079920
PR	31-MAR-1998	98US-0079923
PR	31-MAR-1998	98US-0080105
PR	31-MAR-1998	98US-0080107
PR	31-MAR-1998	98US-0080165
PR	31-MAR-1998	98US-0080194
PR	01-APR-1998	98US-0080327
PR	01-APR-1998	98US-0080328
PR	01-APR-1998	98US-0080332
PR	01-APR-1998	98US-0080349
PR	08-APR-1998	98US-0081034
PR	08-APR-1998	98US-0081070
PR	08-APR-1998	98US-0081071
PR	09-APR-1998	98US-0081191
PR	09-APR-1998	98US-0081203
PR	09-APR-1998	98US-0081229
PR	15-APR-1998	98US-0081817
PR	15-APR-1998	98US-0081838
PR	15-APR-1998	98US-0081952
PR	15-APR-1998	98US-0081955
PR	21-APR-1998	98US-0082565
PR	21-APR-1998	98US-0082569
PR	22-APR-1998	98US-0082700
PR	22-APR-1998	98US-0082704
PR	22-APR-1998	98US-0082767
PR	22-APR-1998	98US-0082796
PR	27-APR-1998	98US-0083336
PR	28-APR-1998	98US-0083392
PR	29-APR-1998	98US-0083422
PR	29-APR-1998	98US-0083495
PR	29-APR-1998	98US-0083496
PR	29-APR-1998	98US-0083499
PR	29-APR-1998	98US-0083500
PR	29-APR-1998	98US-0083545
PR	29-APR-1998	98US-0083554
PR	29-APR-1998	98US-0083598
PR	07-MAY-1998	98US-0084600
PR	07-MAY-1998	98US-0084627
PR	07-MAY-1998	98US-0084637
PR	07-MAY-1998	98US-0084639
PR	07-MAY-1998	98US-0084643
PR	13-MAY-1998	98US-0084643
PR	13-MAY-1998	98US-0085322
PR	13-MAY-1998	98US-0085323
PR	15-MAY-1998	98US-0085339
PR	15-MAY-1998	98US-0085373
PR	15-MAY-1998	98US-0085379
PR	15-MAY-1998	98US-0085580
PR	15-MAY-1998	98US-0085582

PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086466.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH) GENENTECH INC.
XX Wood WT, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPT, 1999-551358/46.
XX N-PSDB; AA234271.
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 12; Fig 183; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA233891 to
XX AA23438, and AA141685 to AA14174 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX Sequence 175 AA;
SQ
Query Match 58.1%; Score 557; DB 20; Length 175;
Best Local Similarity 55.6%; Pred. No. 5,6e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
QY 3 PMTLCRMMSWMLSCIMFLSWVEGESQKRLPSRITCPQGSVAVGYCYSLIILPOTWSN 62
DB 4 PMALPSVSMMLSCILLCQVQGETQKELPSRISCPKSGKAYGSPCYALFLSPKSMMD 63
QY 63 AELSCQMHSGLAFILSTGEITFVSSLVKNLSITAYOYIWIIGLHDPHSHGLTPNGSGMKWS 122
DB 64 ADLACQKRRSGKIVSYLSGAGSFVSSLVRSISNYSITIMIGLHDPYQGSPEPDGSGMWS 123
QY 123 SSNVLTFTYMERNPISIAADRGYCAVLSQKSGFQKWRDNCENELPYICKFK 173
DB 124 STDVVMYFAWEKNPSTILNPGHGSLSRSTGFLKWKDYNCDAKLPYCKFK 174
RESULT 12
ID AAB44311 standard; Protein; 175 AA.
XX AAB44311;
XX AC AAB44311;
XX DT 08-FEB-2001 (first entry)
XX DE Human PRO162 (UNC429) protein sequence SEQ ID NO:452.
XX KM Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.
OS Homo sapiens.

XX WO200053756-A2.
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers I, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kijavini JJ, Kuo SS, Napier MA, Pan J, Paoletti NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
XX WPT, 2000-611443/58.
XX N-PSDB; AAC78569.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
XX Claim 12; Fig 183; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 175 AA;
SQ
Query Match 58.1%; Score 557; DB 21; Length 175;
Best Local Similarity 55.6%; Pred. No. 5,6e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
QY 3 PMTLCRMMSWMLSCIMFLSWVEGESQKRLPSRITCPQGSVAVGYCYSLIILPOTWSN 62
DB 4 PMALPSVSMMLSCILLCQVQGETQKELPSRISCPKSGKAYGSPCYALFLSPKSMMD 63
QY 63 AELSCQMHSGLAFILSTGEITFVSSLVKNLSITAYOYIWIIGLHDPHSHGLTPNGSGMKWS 122
DB 64 ADLACQKRRSGKIVSYLSGAGSFVSSLVRSISNYSITIMIGLHDPYQGSPEPDGSGMWS 123
QY 123 SSNVLTFTYMERNPISIAADRGYCAVLSQKSGFQKWRDNCENELPYICKFK 173
DB 124 STDVVMYFAWEKNPSTILNPGHGSLSRSTGFLKWKDYNCDAKLPYCKFK 174

RESULT 13
AAU29235
ID AAU29235 standard; Protein; 175 AA.
XX
AC AAU29235;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #212.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 15-MAR-2000; 2000US-189328P.
PR 21-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-064484B.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX
PA (GENE) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2001-602746/68.
XX
XX N-PSDB; AAS46136.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the

PT presence of tumours, such as prostate and breast tumours, in mammals and
XX to screen for modulators of the compounds -
XX
PS Claim 11; Fig 424; 774bp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 175 AA;
XX
Query Match 58.1%; Score 557; DB 22; Length 175;
Best Local Similarity 55.6%; Pred. No. 5,6e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
XX
OY 3 PMLCRMSWMLSLCLMFLSVVEGESOKLPPSRITCPGSAVAYGYCYSLILIPOTWSN 62
|| : ||||| : || : ||||| : || : ||||| : || : ||||| : || : ||||| :
Db 4 PMALPSVSWMLSLCLILICVOGETOKELPPSRISCPKSGKAYGCVYALFLPSKSWMD 63
XX
OY 63 AELSCOMHSGHIAFLSTGRTFVSVSLVKNKSLTAYOYIWIHDPHSHGLPNSGGMKNS 122
|| : ||||| : || : ||||| : || : ||||| : || : ||||| : || : ||||| :
Db 64 ADLACQKRPSCGLVSVLSGAEGRSVSVLSINSISYITWIGLHDPGSEPPGDGEMNS 123
|| : ||||| : || : ||||| : || : ||||| : || : ||||| : || : ||||| :
OY 123 SSNVLFYFNWERNPISIAADRCYCAVLSOKSGFQKRDENCENELPYCKEK 173
|| : ||||| : || : ||||| : || : ||||| : || : ||||| : || : ||||| :
Db 124 STDVNYFAMEKNPSTILINPHGCSLSRSTGFLKWKDYNDARLPYCKEK 174
XX
RESULT 14
ABR95482
ID ABR95482 standard; Protein; 175 AA.
XX
AC ABR95482;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO162 SEQ ID NO: 120.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiatic; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.

A:Note: only Intron/exon boundaries are shown; exon I and the beginning of exon II are
 ension of the open reading frame to an AUG codon in exon I is shown in accession A59313
 R:Ussetti, N.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
 submitted to Genbank, August 1993
 A:Reference number: A59313
 A:Accession: A59313
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: MMKRV',1-175 <DUS2>
 A:Cross-references: GB:U07127; NID:g349550; PIND:AAA41805.1; PID:g349551
 A:Note: an incorrect initiation codon was used
 R:Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dagorn
 A:Title: PAV, a pancreatic secretory protein induced during acute pancreatitis, is expre
 A:Reference number: I51899; MUID:94056762; PMID:8238345
 A:Accession: I51899
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-175 <IOV1>
 A:Cross-references: GB:M8049; NID:g393210; PIND:AAA16341.1; PID:g393211
 A:Note: in Genbank entry RAHPAC, release 113.0, the source is designated as Rattus rattus
 R:Kamimura, T.; West, C.; Beutler, E.
 Gene 118, 299-300, 1992
 A:Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
 A:Reference number: JCI257; MUID:92380521; PMID:1511905
 A:Accession: JCI257
 A:Molecule type: mRNA
 A:Residues: 1-6,'5',8-175 <RAM>
 A:Cross-references: GB:543715; NID:g254694; PIND:RAM23103.1; PID:g254695
 R:Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
 J. Biol. Chem. 266, 24664-24669, 1991
 A:Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a
 A:Reference number: A41719; MUID:92105133; PMID:1722211
 A:Accession: A41719
 A:Molecule type: mRNA
 A:Residues: 1-175 <IOV2>
 A:Cross-references: GB:M5149; NID:g206030; PIND:AAA41807.1; PID:g206031
 A:Note: the amino-terminal residue of the mature protein was identified as Glu
 A:Gene: pap
 A:Genetics:
 A:Introns: 26/1; 65/3; 111/3; 154/1
 A:Note: the first intron occurs before the initiator codon
 C:Superfamily: tetranectin; C-type lectin homology
 C:Keywords: lectin; pancreas
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-175/Product: pancreatitis-associated protein #status experimental <MAT>
 F:40-171/Domain: C-type lectin homology <KCH>
 F:40-51,68-171,146-163/Disulfide bonds: #status predicted
 Query Match 61.9%; Score 593; DB 2; Length 175;
 Best Local Similarity 61.0%; Pred. No 3,9e-47;
 Matches 100; Conservative 30; Mismatches 34; Indels 0; Gaps 0;
 Oy - 9 MSWMLSCIMPLSWEGESQKIPSPSRITCPQGSVAVGYCYCSLILIPQWMAELSCQ 68
 Db 10 MSWMLSCIMLISQYGEDSPKIPSPARISCPKGSQAYALFQIPQWFDLACQ 69
 Oy 69 MHFSCHLAFLLSTGCTIVSSLYKNSLTAQYIWIGLDPSHGLPLNCSGMWSSSNVLT 128
 Db 70 KRPSCHLAVSLVNAASPLASVKNKNGNSYOTIWIGLDPTLGGHPNGGWMNSNDIMN 129
 Oy 129 FYNWMRNPISIAADRCYCAVLISQSGFQKWRDFNCENELPYICKF 172
 Db 130 FYNWMRNPSTALDRFGCSLSSSGFLMRDRDTTCVAKLPYCKF 173
 RESULT 3
 A49616
 pancreatitis-associated protein precursor - human
 N:Alternate names: C-type lectin; pancreatic stone protein homolog HIP
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
 C:Accession: A49616; A44931; S29821; S48197; I55580

```

R:Russett, N.J.; Fritgerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J., 1994
Genomics 19, 108-114, 1994
A>Title: Molecular cloning, genomic organization, and chromosomal localization of the
A:Reference number: A49616; MUID:94245143; PMID:8188210
A:Accession: A49616
A:Molecule type: DNA
A:Residues: 1-175 <DMS>
A:Cross-references: GB:JL15533; NID:g482908; PIND:AAA60020.1; PID:g482909
R:Lasserre, C.; Christa, L.; Simon, M.T.; Venier, P.; Brecht, C.
Cancer Res. 52, 5089-5095, 1992
A>Title: A novel gene (HIP) activated in human primary liver cancer.
A:Reference number: A44931; MUID:92386513; PMID:1325231
A:Accession: A44931
A:Molecule type: mRNA
A:Residues: 1-175 <LAS>
A:Cross-references: GB:R68641; NID:g312806; PIND:CAA46605.1; PID:g312807
A:Experimental source: hepatocellular carcinoma
A>Note: Sequence extracted from NCBI database (NCBIN:113007, NCBIPI:113008)
R:Ritch, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A>Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homo
A:Reference number: S29821; MUID:93176807; PMID:7679928
A:Accession: S29821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-175 <TIO>
A:Cross-references: GB:DJ3510; NID:g285970; PIND:BA02728.1; PID:g285971
R:Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Ve
Eur. J. Biochem. 224, 29-38, 1994
A>Title: Structural organization and chromosomal localization of a human gene (HIP/PA
A:Reference number: S48197; MUID:94357223; PMID:8076648
A:Accession: S48197
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <LA2>
R:Orreile, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
J. Clin. Invest. 90, 2284-2291, 1992
A>Title: Human pancrreticitis-associated protein. Messenger RNA cloning and expression
A:Reference number: I55580; MUID:93107309; PMID:1469087
A:Accession: I55580
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <RES>
A:Cross-references: GB:S51768; NID:g262368; PIND:AAB24642.1; PID:g262369
C:Genetics:
A:Gene: GDB:PAP; HIP
A:Cross-references: GDB:136839; OMIM:167805
A:Map position: 2p12-2p12
A:Introns: 26/1; 65/3; 111/3; 154/1
C:Keywords: acute phase; extracellular protein; pancreas
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-173/Product: pancrreticitis-associated protein #status predicted <MAT>
F.40-51,68-171,146-163/Disulfide Bonds: #status predicted
Query Match 59.7%; Score 572; DB 2; Length 175;
Best local similarity 57.6%; Pred. No. 3,3e-45;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;
3 PMTLCRMGSMILLSCMLPTLSWGEESQRLKLPSSRTICPOGSVAVGYCYSLILIPQWNS 62
|||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4 PMALPSVSMILLSCMLTSLNOYGEQRELPASRIRCPKSKAYASHCYALFLSPKSWTD 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 AELSCQMFHSGLAALLTSGETTPVSSLVKNSLTAYQIWIYGLHDPHSIGTLPNCSGKQWS 122
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 64 ADLAQQRKPSGLVSLVSGAEGSFVSSLYKNSYVWVGLHDPTGGTEPNGEQWMS 123
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 SSNTLFYWERNPSTIADRCYCAVLSCGSGFOKRDRCNEHLPYICKF 172
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 124 SSDVNNYFAMERNPSTISSPGHCASTLRSTAFELRKADYINCVRLLPYCKF 173

```

RESULT 4

A37194

pancreatic thread protein precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999

C:Accession: A37194; A53897

R:de la Monte, S.M.; Ozuturk, M.; Wands, J.R.

J. Clin. Invest. 86, 1004-1013, 1990

A:Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease and

A:Reference number: A37194; MUID:90368981, PMID:2394826

A:Accession: A37194

A:Molecule type: mRNA

A:Residues: 1-175

A:Cross-references: GB:M59794; NID:g163648; PIDN:AAA30750.1; PID:g163649

R:Cal, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabbs, J.W.

J. Protein Chem. 9, 623-632, 1990

A:Title: Structural analysis of bovine pancreatic thread protein.

A:Reference number: A53897; MUID:91197388; PMID:2085387

A:Accession: A53897

A:Molecule type: protein

A:Residues: 38-138;141-175 <CAI>

C:Comment: The purified protein undergoes a reversible globule-fibril transformation and

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: disulfide bond; extracellular protein; pancreas

F:38-138/Product: pancreatic thread protein chain A #status experimental <ACH>

F:141-175/Product: C-type lectin homology <LCH>

F:141-175/Product: pancreatic thread protein chain B #status experimental <BCH>

Query Match

Best Local Similarity 55.5%; Score 531.5; DB 2; Length 175;

Matches 94; Conservative 32; Mismatches 46; Indels 1; Gaps 1;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSAVAGSYCYSLILIPQT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGNSOKLPSPARISCSGSMAYRSHCYALPKPKPT 60

QY 60 WSNALSCOMHPSGHLAFLSTGETTFVSSLVKNLSLTAAYQYIWIIGLHDPHSGTLPNCSGW 119

DB 61 WMDADLACQKRRSGHVLSTLSGSEAFVSLVNRNMLNTOSDIWIIGLHDPHSGTLPNCSGW 120

QY 120 KMSSSNVLTFFYWMERNPSIAADRGYCAVLSCSGQKRPQKRDNCENELPYICKK 172

DB 121 EWSNDVLYNVTYMETDPAISPGYCSLSRSSGYLKRMDHNCMLNLPYCKK 173

Query Match

Best Local Similarity 49.5%; Score 474; DB 2; Length 174;

Matches 89; Conservative 30; Mismatches 53; Indels 2; Gaps 2;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSAVAGSYCYSLILIPQT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGNSOKLPSPARISCSGSMAYRSHCYALPKPKPT 60

QY 60 WSNALSCOMHPSGHLAFLSTGETTFVSSLVKNLSLTAAYQYIWIIGLHDPHSGTLPNCSGW 119

DB 61 WMDADLACQKRRSGHVLSTLSGSEAFVSLVNRNMLNTOSDIWIIGLHDPHSGTLPNCSGW 120

QY 120 KMSSSNVLTFFYWMERNPSIAADRGYCAVLSCSGQKRPQKRDNCENELPYICKK 172

DB 121 EWSNDVLYNVTYMETDPAISPGYCSLSRSSGYLKRMDHNCMLNLPYCKK 173

Query Match

Best Local Similarity 52.9%; Score 518; DB 2; Length 174;

Matches 92; Conservative 39; Mismatches 41; Indels 2; Gaps 2;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSAVAGSYCYSLILIPQT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGNSOKLPSPARISCSGSMAYRSHCYALPKPKPT 60

QY 60 WSNALSCOMHPSGHLAFLSTGETTFVSSLVKNLSLTAAYQYIWIIGLHDPHSGTLPNCSGW 119

DB 61 WMDADLACQKRRSGHVLSTLSGSEAFVSLVNRNMLNTOSDIWIIGLHDPHSGTLPNCSGW 120

Query Match

Best Local Similarity 51.1%; Score 518; DB 2; Length 174;

Matches 89; Conservative 30; Mismatches 53; Indels 2; Gaps 2;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSAVAGSYCYSLILIPQT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGNSOKLPSPARISCSGSMAYRSHCYALPKPKPT 60

RESULT 6

I83377

regenerating protein III (reg III) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999

C:Accession: I60296; I83377

R:Suzuki, Y.; Yonekura, H.; Watanabe, T.; Uno, M.; Morizumi, S.; Miyashita, H.; Oka

Gene 144, 315-316, 1994

A:Title: Structure and expression of a novel rat RegIII gene.

A:Reference number: I60296; MUID:94314238; PMID:8039722

A:Accession: I60296

A:Molecule type: mRNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

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A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

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A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

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A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

RESULT 7

A48689

pancreatitis-associated protein PAP-3 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A48689

R:Frigerio, J.M.; Dusetti, N.J.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.

Biochemistry 32, 9236-9241, 1993

A:Title: Identification of a second rat pancreatitis-associated protein. Messenger RN

A:Reference number: A48689; MUID:93378571; PMID:8369291

A:Accession: A48689

A:Molecule type: mRNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Cross-references: GB:M18963; NID:q190978; PIDN:AAA36558.1; PII

Db 68 NSGNLVSILTQAECAFVASLIKESGTDDEFNWIGLHDPK-----KNRRHWSSGSLVSYK 122

Wed Apr 16 12:14:49 2003

us-08-401-530-2.rpr

Page 7

[illegible]

Search completed: April 16, 2003, 10:47:46
Job time : 18 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:41:05 ; Search time 12 Seconds

(without alignments)
601.407 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 958
Sequence: 1 MLPMTLCRMSMLSLCLMFL.....QKWRDRCENELPYCKFKV 174

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958	100.0	175	1	PGCG_HUMAN
2	605.5	63.2	175	1	PAP1_MOUSE
3	593	61.9	175	1	PAP1_RAT
4	572	59.7	175	1	PAP1_HUMAN
5	531.5	55.5	175	1	LITH_BOVIN
6	525.5	54.9	175	1	PAP2_MOUSE
7	518	54.1	174	1	PAP3_MOUSE
8	518	54.1	174	1	PAP3_RAT
9	466	48.6	174	1	PAP2_RAT
10	402.5	42.0	166	1	LITH_HUMAN
11	395.5	41.3	165	1	LITH_RAT
12	386.5	40.3	173	1	LITH_PIG
13	386	40.3	173	1	LITH_MOUSE
14	385.5	40.2	166	1	LITH_HUMAN
15	380.5	39.7	165	1	LITH_MOUSE
16	192	20.0	134	1	ABAB_TRIAB
17	191	19.9	134	1	ABAB_TRIAB
18	188	19.6	158	1	LECG_TRIST
19	176	18.4	146	1	IXR_TRIFL
20	176	18.4	152	1	IXA_TRIFL
21	172	18.0	133	1	ECHA_ECHA
22	171.5	17.9	135	1	LECG_CROAT
23	171	17.8	1458	1	PAZR_RABIT
24	165	17.2	132	1	ABBA_TRIAB
25	164.5	17.2	2109	1	PGCA_CHICK
26	158	16.5	125	1	ABAB_TRIAB
27	156	16.3	132	1	ACAL_ANSAN
28	155.5	16.2	162	1	LECG_MEGRO
29	153	16.0	133	1	RHCA_MEGRO
30	152.5	15.9	1268	1	PGCN_MOUSE
31	152.5	15.9	2364	1	PGCA_BOVIN
32	152	15.9	123	1	ABAB_TRIAB
33	150.5	15.7	2415	1	PGCA_HUMAN

34	150.5	15.7	3562	1	PGCV_CHICK	Q09053	gallus gall
35	149.5	15.6	1257	1	PGCN_RAT	P55067	rattus norv
36	149.5	15.6	2132	1	PGCA_MOUSE	Q61282	mus muscicu
37	149.5	15.6	2738	1	PGCV_RAT	Q9874	rattus norv
38	149.5	15.6	3358	1	PGCV_MOUSE	P62059	mus muscicu
39	149.5	15.6	3396	1	PGCV_HUMAN	P13611	homo sapien
40	148.5	15.5	1456	1	MANR_HUMAN	P22837	homo sapien
41	147.5	15.4	2124	1	PGCA_RAT	P07857	rattus norv
42	147.5	15.4	3381	1	PGCV_BOVIN	P81282	bos taurus
43	146	15.2	1463	1	PAZR_BOVIN	P49259	bos taurus
44	142.5	14.9	2333	1	PGCA_CANPA	Q28343	canis fami
45	135.5	14.1	166	1	TETN_CARSP	P26258	caracharhin

ALIGNMENTS

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RESULT 1
ID      PGCG_HUMAN      STANDARD:      PRT: 175 AA.
AC      Q92778; P70109;
DT      15-JUL-1998 (rel. 36, Created)
DI      30-MAY-2000 (rel. 39, last sequence update)
DE      15-JUN-2002 (rel. 41, last annotation update)
DE      Pancreatic beta cell growth factor precursor (Islet neogenesis
DE      associated protein).
GN      INGPAP.
OS      Homo sapiens (Human), and
OS      Mesocricetus auratus (Golden hamster).
OC      Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606, 10036;
RN      [1]
RP      SEQUENCE FROM N.A., AND SYNTHESIS OF 104-118.
RC      STRAIN=Lake View Golden; TISSUE=Pancreas;
RX      MEDLINE=97296198; PUBMED=9151782;
RA      Ratelaof R., Piltenger G.L., Barlow S.W., Qin X.F., Yan B.,
RA      Rosenberg L., Duguid W.P., Vlnik A.I.;
RT      "Cloning and sequencing of the pancreatic islet neogenesis associated
RT      protein (INGAP) gene and its expression in islet neogenesis in
RT      hamsters."
RT      J. Clin. Invest. 99:2100-2109(1997).
RL      -1-
RC      FUNCTION: CONSTITUENT OF ILIOTROPIN, WHICH IS A PARTIALLY PURIFIED
RC      PREPARATION OF CELLOPHANE WRAPPING (CW) PANCREATA. CAPABLE OF
RC      INITIATING DOCT CELL PROLIFERATION, A PRENEOPLASTIC FOR ISLET
CC      NEOGENESIS.
CC      -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC      -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN CW ANIMALS PANCREAS AND TO A
CC      LESSER EXTENT IN DODGENDUM. IN PANCREAS IT IS FOUND IN ACINAR
CC      CELLS, BUT NOT IN ISLET.
CC      -1- INDUCTION: FOUND 1 AND 2 DAYS AFTER CELLOPHANE WRAPPING, ABSENT BY
CC      THE 6TH DAY. THIS PERIOD COINCIDES WITH ISLET NEOGENESIS.
CC      -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC      -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-2 OR MET-5 IS THE
CC      INITIATOR.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: U41737; ABAB6497.1; ALT_INIT.
DR      EMBL: U41738; ABAB6754.1; ALT_INIT.
DR      HSSP: P05451; 10DD.
DR      InterPro: IPR000282; CytoK_receptor_2.
DR      InterPro: IPR001304; Lectin_C.
DR      InterPro: IPR003990; Pancreatis_ac.
DR      Pfam: PF00059; lectin_c_1.
DR      PRINTS: PR01504; PNCREATITISAP.
DR      SMART: SM00034; CLECT; 1.

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DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19940 MW; 3854F36BA35D17CE CRC64;

Query Match 100.0%; Score 958; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.8e-76;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPMTLCRMSNMWLSCLMFLSWEGEESQKRLPSRITCPQGSVAYGSCYSLIIPQTW 60
DB 2 MLPMTLCRMSNMWLSCLMFLSWEGEESQKRLPSRITCPQGSVAYGSCYSLIIPQTW 61
OY 61 SNAELSCQMHPGSHLAFLSTGEITFVSLYKNSLTAYOYIWIHGLHDSHGTLPMGSGWK 120
DB 62 SNAELSCQMHPGSHLAFLSTGEITFVSLYKNSLTAYOYIWIHGLHDSHGTLPMGSGWK 121
OY 121 WSSSNVLTFFYMWERNPSTIADRGCAVLSQKSGFQKWRDPCNENELPYICKFKV 174
DB 122 WSSSNVLTFFYMWERNPSTIADRGCAVLSQKSGFQKWRDPCNENELPYICKFKV 175

RESULT 2
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AC P35230;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
GN PAPI OR PAP OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Small intestine;
RX MEDLINE=93176807; PubMed=7679928;
RA Itoh T., Terada H.;
RT "Cloning and tissue-specific expression of cDNAs for the human and
RT mouse homologues of rat pancreatitis-associated protein (PAP).";
RL Biochim. Biophys. Acta 1172:184-186(1993).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=97208868; PubMed=9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
CC BACTERIAL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
CC PANCREATIC ACINAR CELLS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL
CC INTESTINE. MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
CC HEALTHY PANCREAS.
CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
CC PANCREATIC INFLAMMATION.
CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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CC -----
DR EMBL; D13509; BAA02727.1; -
DR EMBL; D63359; BAA18928.1; -
DR EMBL; D63360; BAA18929.1; -
DR PIR; S29822; S29822.
DR HSSP; P05451; ILIT.
DR MGD; MGI:97478; Pap.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin.c1.
DR PRINTS; PR01504; PNCREATITISAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 63.2%; Score 605.5; DB 1; Length 175;
Best Local Similarity 60.7%; Pred. No. 1.7e-45;
Matches 105; Conservative 29; Mismatches 36; Indels 1; Gaps 1;

OY 1 MLPMTLCR-MSNMWLSCLMFLSWEGEESQKRLPSRITCPQGSVAYGSCYSLIIPQT 59
DB 1 MLPMTLCRMSNMWLSCLMFLSWEGEESQKRLPSRITCPQGSVAYGSCYSLIIPQT 60
OY 60 WSNELSCQMHPGSHLAFLSTGEITFVSLYKNSLTAYOYIWIHGLHDSHGTLPMGSGWK 119
DB 61 WSNELSCQMHPGSHLAFLSTGEITFVSLYKNSLTAYOYIWIHGLHDSHGTLPMGSGWK 120
OY 120 WSSSNVLTFFYMWERNPSTIADRGCAVLSQKSGFQKWRDPCNENELPYICKFKV 172
DB 121 WSSSNVLTFFYMWERNPSTIADRGCAVLSQKSGFQKWRDPCNENELPYICKFKV 173

RESULT 3
PAP1_RAT STANDARD; PRT; 175 AA.
AC P25031; 064231; 064102;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (Peptide 23) (REG-2).
GN PAPI OR PAP OR REG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-39.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
RX MEDLINE=92105133; PubMed=1722211;
RA Iovanna J., Orelle B., Kelm V., Dagnon J.-C.;
RT "Messenger RNA sequence and expression of rat pancreatitis-associated
RT protein, a lectin-related protein overexpressed during acute
RT experimental pancreatitis.";
RL J. Biol. Chem. 266:24664-24669(1991).
RN RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=9405672; PubMed=8238345;
RA Iovanna J.L., Kelm V., Bosshard A., Orelle B., Frigerio J.M.,
RA Dusetti N., Dagnon J.C.;

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RT PAP, a pancreatic secretory protein induced during acute
 RT pancreatitis, is expressed in rat intestine.;
 RL Am. J. Physiol. 265:G611-G618(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mistral; TISSUE-Liver;
 RX MEDLINE-93300847; PubMed-8314803;
 RA Dusetti N.J., Frigerio J.M., Kelm V., Dagorn J.C., Iovanna J.;
 RT "Structural organization of the gene encoding the rat pancreatitis-
 RT associated protein. Analysis of its evolutionary history reveals an
 RT ancient divergence from the other carbohydrate-recognition domain-
 RT containing genes.";
 RL J. Biol. Chem. 268:14470-14475(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92380521; PubMed-1511905;
 RA Kamimura T., West C., Reutler E.;
 RT "Sequence of a cDNA clone encoding a rat Reg-2 protein.";
 RL Gene 118:299-300(1992).
 RN [5]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Sprague-Dawley; TISSUE-Pituitary;
 RX MEDLINE-95203187; PubMed-7895644;
 RA Katumata N., Chakraborty C., Nyal Y., Schroeder I.C.,
 RT Murphy L.J., Shu R.P., Friesen H.G.;
 RT "Molecular cloning and expression of peptide 23, a growth hormone-
 RT releasing hormone-inducible pituitary protein.";
 RL Endocrinology 136:1332-1339(1995).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION. SECRETED ALSO BY PITUITARY CELLS. THE
 CC SECRETION THERE IS STIMULATED BY GH-RELEASING HORMONE AND
 CC INHIBITED BY SOMATOSTATIN.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M55149; AAA41807.1; -;
 DR EMBL: M98049; AAA16341.1; -;
 DR EMBL: L07127; AAA41805.1; ALT_INIT.
 DR EMBL: S43715; AAB23103.1; -;
 DR EMBL: S77413; AAB33848.2; -;
 DR FIR: A41719; A41719.
 DR HSSP: P05451; 10DD.
 DR InterPro: IPR001304; LECTIN_C.
 DR InterPro: IPR003990; Pancreatis-ac.
 DR Pfam: PF00059; lectin_c.1.
 DR PRINTS: PR01504; PNCREATITISAP.
 DR SMART: SM00034; CLECT. 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 KW Signal; Lectin; Inflammatory response; Acute phase.
 FT SIGNAL 1 26
 FT CHAIN 175
 FT DOMAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
 FT DISULFID 38 173 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 FT CONFLICT 7 163 F->S (IN REF. 4).
 FT CONFLICT 123 123 S->T (IN REF. 5).
 SQ SEQUENCE 175 AA; 19617 MW; C43892BF31B0B525 CRC64;

Query Match 61.9%; Score 593; DB 1; Length 175;
 Best Local Similarity 61.0%; Pred. No. 2,1e-44;
 Matches 100; Conservative 30; Mismatches 34; Indels 0; Gaps 0;
 Oy 9 MSWMLSCIMFLSWVEGEESQKRLPSRITPCPGSVAYGSCYSLILIPQWNAELSCQ 68
 Db 10 MSWMLSCIMFLSWVEGEESQKRLPSRITPCPGSVAYGSCYSLILIPQWNAELSCQ 69
 Oy 69 MHSGLAFLSTGEITFVSLYKNSLITAYQYTWIGLHPSPGTLPNSGKWKSSNVLT 128
 Db 70 KRPGCHLVSYLVNAEASFSLAMKNGNSYQYTWIGLHPSPGTLPNSGKWKSSNVLT 129
 Oy 129 FYNERNPSIADRGYCAVLGSKSGFGKMRDFNCENELPYCKF 172
 Db 130 YVNERNPSTALDRGFCGSLSRSSGFLMRMDTCEVKLPYCKF 173
 RESULT 4
 PAPI_HUMAN STANDARD; PRT; 175 AA.
 AC 006141;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pancreatitis-associated protein 1 precursor.
 GN PAPI OR PAP OR HIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pancreas; and Small intestine;
 RX MEDLINE-93176807; PubMed-7679928;
 RA Itoh T., Teroka H.;
 RT "Cloning and tissue-specific expression of cDNAs for the human and
 RT mouse homologues of rat pancreatitis-associated protein (PAP).";
 RL Biochim. Biophys. Acta 1172:184-186(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pancreas;
 RX MEDLINE-93107309; PubMed-1469087;
 RA Orelle B., Kelm V., Masciotra L., Dagorn J.-C., Iovanna J.-L.;
 RT "Human pancreatitis-associated protein. Messenger RNA cloning and
 RT expression in pancreatic diseases.";
 RL J. Clin. Invest. 90:2284-2291(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-92386513; PubMed-1325291;
 RA Lasserre C., Christa L., Simon M.T., Vernier P., Brechot C.;
 RT "A novel gene (HIP) activated in human primary liver cancer.";
 RL Cancer Res. 52:5089-5095(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE-94245143; PubMed-8188210;
 RA Dusetti N.J., Frigerio J.M., Fox M.F., Swallow D.M., Dagorn J.C.,
 RT Iovanna J.L.;
 RT "Molecular cloning, genomic organization, and chromosomal
 RT localization of the human pancreatitis-associated protein (PAP)
 RT gene.";
 RL Genomics 19:108-114(1994).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE. LOW
 CC EXPRESSION IS FOUND IN HEALTHY PANCREAS.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS AND
 CC IN SOME PATIENTS WITH CHRONIC PANCREATITIS.

D6		121	EMNSDVIANLNNDGDPSTVNRHGCGSLTASSGFLAKMGDYCDGLTFPCFKR	174
<hr/>				
	RESULT 7			
PAP3_MOUSE				
ID	PAP3_MOUSE	STANDARD:	PRT;	174 AA.
AC	009049;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Pancreatitis-associated protein 3 precursor (REG III-gamma).			
GN	PAP3 OR REG3G.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-C57BL/6J; TISSUE=Liver and Pancreas;			
RX	MEDLINE=97208868; PubMed=9055810;			
RA	Narusuhima Y., Unno M., Nakagawa K.-I., Mori M., Miyashita H.,			
RA	Suzuki Y., Noguchi N., Takasawa S., Kunagai T., Yonekura H.,			
RA	Okamoto H.;			
RT	"structure, chromosomal localization and expression of mouse genes			
RL	encoding type III Reg, RegIII alpha, RegIII beta, RegII gamma.";			
RL	Gene 185:155-168(1997).			
CC	-1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF			
CC	BACTERIAL PROLIFERATION.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL			
CC	INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN			
CC	HEALTHY PANCREAS.			
CC	-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	-----			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; D63361; BAA18930.1; .			
DR	EMBL; D63362; BAA18931.1; .			
DR	HSSP; P05451; LIIT			
DR	MGI; MGI:109406; Reg3g.			
DR	Iinterpro; IPR001304; Lectin_C.			
DR	Iinterpro; IPR003990; PancreatIs.ac.			
DR	Pfam; PF00059; lectin_c_1.			
DR	PRINTS; PR01504; PNCREAITSAP.			
DR	SMART; SM00034; GLECT; 1.			
DR	PROSITE; PS00615; C_Type_Lectin_1; FALSE_NEG.			
DR	PROSITE; PS50041; C_Type_Lectin_2; 1.			
KM	Signal; Lectin; Inflammatory response; Acute phase; Multigene family.			
FT	signal	1	26	POTENTIAL.
FT	CHAIN	27	174	PANCREATITIS-ASSOCIATED PROTEIN 3.
FT	DOMAIN	38	172	C-TYPE LECTIN (LONG FORM).
FT	DISULEID	40	51	BY SIMILARITY.
FT	DISULEID	68	170	BY SIMILARITY.
FT	DISUREID	145	162	BY SIMILARITY.
SO	SEQUENCE	174 AA;	19307 MW;	5575E9E36AD8CF CRC64;
<hr/>				
	Query Match	54.1%;	Score 518;	DB 1; Length 174;
	Best Local Similarity	53.4%;	Pred. NO. 5.9e-38;	
	Matches 93;	Conservative 35;	Mismatches 44;	Indels 2; Gaps 2;
OY	1 MLP-MTLCRSMWLLSCLEFELSWVEGESEOKKLBSRRTCPOGSVAAGSYCYLIIPQT	59		
	: : : : : : : : : : : : : : : : :			
Db	1 MLPTITTIMSNMLLSCLMLLSOVQGVPAKKDAPSPSRSCCKSGRAIGCVALLFEVSKN	60		
	: : : : : : : : : : : : : : : : :			
OY	60 WSNALHSCMHFGHLAFLLSTGCETFPSSLVKKSLRAYOYTMTGLDSPGHGLPNNGSQ	119		
	: : : : : : : : : : : : : : : : :			
Db	61 WTADAMACKORPSGVLNVSLGAENSAFLSSMIKSGNSGGYWLGHDPLTGAEPPRGGM	120		

RESULT 8	PAP3_RAT	STANDARD;	PRT;	174 AA.
ID	PAP3_RAT			
AC	P42854;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Pancreatitis-associated protein 3 precursor.			
GN	PAP3.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-Sprague-Dawley; TISSUE=Intestine;			
RA	MEDLINE=94060113; PubMed=8241280;			
RX	Frigieri J.-M., Dusetil N.J., Garrido P., Dagorn J.C., Iovanna J.L.,			
RT	"The pancreatitis associated protein III (PAP III), a new member of			
RL	the PAP gene family.";			
CC	Biochim. Biophys. Acta 1216:329-331(1993).			
CC	-1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF			
CC	BACTERIAL PROLIFERATION.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; L20696; AAA41809.1; -			
DR	EMBL; U09193; AAA79231.1; -			
DR	HSP; F03451; L11T.			
DR	InterPro; IPR001304; Lectin_C.			
DR	InterPro; IPR003990; Pancreatis_ac.			
DR	Pfam; PF00059; lectin_c_1.			
DR	PRINTS; PR01504; PNCREATITISAP.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.			
DR	PROSITE; PS50041; C-TYPE LECTIN_2; 1.			
KW	Signal; Lectin; Inflammatory response; Acute phase.			
FT	SIGNAL 1 26			
FT	CHAIN 27 174			
FT	DOMAIN 38 172			
FT	DISULFID 40 51			
FT	DISULFID 68 170			
FT	DISULFID 145 162			
FT	SEQUENCE 174 AA; 19143 MW; 5CED2EB87C46E45C CRC64;			
SO	SEQUENCE			
Query Match	54.1%; Score 518; DB 1; Length 174;			
Best Local Similarity	52.9%; Pred. No. 5; 9e-38;			
Matches 92; Conservative 39; Mismatches 41; Indels 2; Gaps 2;				
OY	1 MUP-MULCRMSMWLSCIMFLSWVEEESOKKIPSSRINCPQSSVAYGCTSLIIPOT 59			
DB	1 MPRVALTTTSMWLSLIMLSOVQGEADAEVDPTRISCPKSRAYGCTALAEVSYS 60			
OY	60 WSNAEISQCMHFGSHLAFLLSTGEITFVSSLYVNSLTAFOYIWIIGLHPSHGTLPNGSGM 119			
DB	61 WFPADLACQKRGPHGLVSVLSGSEASPVSLIKSSGNSGQVMWIGLHDPFLGEPNPGW 120			
OY	120 KWSSSNVLTFFYNNERRPSTIADNGYCAVLSQKSGFQKMRDFNENLPTCYCKRK 173			

Db	121	EMSNADVANNYNNENWENPS-SVSGSHCGCLTFRASGFLMRRENMCISLPPYCKFK	173
RESULT 9			
PAP2_RAT			
ID	PAP2_RAT	STANDARD:	PRT: 174 AA.
AC	P35231:		
DR	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet of Langerhans regenerating protein 3) (REG 3).		
GN	PAP2 OR REG3.		
OS	Rattus norvegicus (Rat).		
OC	Eumariota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RX	MEDLINE=93378971; PubMed=8369291;		
RA	Frigerio J.-M., Duseti N.J., Kelm V., Dagorn J.C., Iovanna J.L.;		
RT	"Identification of a second rat pancreatitis-associated protein."		
RT	Messenger RNA cloning, gene structure, and expression during acute pancreatitis."		
RL	Biochemistry 32:9236-9241(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Mistart;		
RA	MEDLINE=94314238; PubMed=8039722;		
RT	Suzuki Y., Yonekura H., Watanabe T., Unno M., Morizumi S.,		
RT	Miyashita H., Okamoto H.;		
RL	"Structure and expression of a novel rat RegII gene."		
RL	Gene 144:315-316(1994).		
CC	-I- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF BACTERIAL PROLIFERATION.		
CC	-I- SUCCERULAR LOCATION: Secreted.		
CC	-I- TISSUE SPECIFICITY: LOW EXPRESSION FOUND IN HEALTHY PANCREAS.		
CC	-I- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC INFLAMMATION.		
CC	-I- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.		
CC	-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.		
CC	-----		
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CC	-----		
DR	EMBL: L10230; AAA1808.1; -		
DR	EMBL: L10229; AAA02980.1; -		
DR	EMBL: D26078; BAA05071.1; -		
DR	EMBL: D26076; BAA04904.1; -		
DR	PIR: A48689; A48689.		
DR	HSSP: P05451; LITR.		
DR	InterPro: IPR001304; lectin.C.		
DR	InterPro: IPR003980; Pancreatis.ac.		
DR	Pfam: PF00059; lectin.C; 1.		
DR	PRINTS: PR01504; PANCREATITISAP.		
DR	SMART: SM00034; CLECT; 1.		
DR	PROSITE: PS00615; C.TYPE_LECTIN_1; 1.		
DR	PROSITE: PS50041; C.TYPE_LECTIN_2; 1.		
KW	Signal, lectin; Inflammatory response; Acute phase.		
FT	SIGNAL 1 25		
FT	CHAIN 174		
FT	DOMAIN 37 172		
FT	DISULEID 39 50		
FT	DISULEID 67 170		
FT	DISULEID 145 162		
FT	CONFLICT 104 104		
FT	CONFLICT 174 AA; 19599 MW; 4530EB84496E5088 CRC64;		
SEQUENCE			

LIT1_MOUSE STANDARD; PRT; 165 AA.
ID LIT1_MOUSE
AC P43137;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lithostathine 1 precursor (Pancreatic stone protein 1) (PSP)
DE (Pancreatic thread protein 1) (PTP) (Islet of Langerhans regenerating
DE protein 1) (REG 1).
GN REG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC -STRAIN=C57BL/6J;
RX MEDLINE=93340209; PubMed=8340418;
RA Uno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H.,
RA Morizumi S., Okamoto H., Itoh T., Terakura H.,
RT "Structure, chromosomal localization, and expression of mouse reg
RT genes, reg I and reg II. A novel type of reg gene, reg II, exists in
RT the mouse genome."
RL J. Biol. Chem. 268:15974-15982(1993).
CC -I- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CC CARBONATE PRECIPITATION.
CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND
CC NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS.
CC EXPRESSED STRONGLY IN PANCREAS, MODERATELY IN GALLBLADDER, AND
CC WEAKLY IN LIVER.
CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D14010; BAA03111.1; -.
DR HSSP: P05451; LIT1.
DR MGD: MG1:97895; Reg1.
DR InterPro: IPR003990; Lectin_C.
DR InterPro: IPR003990; PancreatIs_ac.
DR Pfam: PF00059; Lectin_Cf_1.
DR PRINTS: PR01504; PNCREATITSAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW Glycoprotein; Signal; Lectin.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 1 165 LITHOSTATHINE 1.
FT DOMAIN 33 163 C-TYPE LECTIN (LONG FORM).
FT DISULFID 35 46 BY SIMILARITY.
FT DISULFID 63 161 BY SIMILARITY.
FT DISULFID 136 153 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GlcNAc...) (POTENTIAL).
SQ SEQUENCE 165 AA; 18518 MW; 2950174AF5D666BA CRC64;

Query Match 39.7%; Score 380.5; DB 1; Length 165;
Best Local Similarity 42.3%; Pred. No. 3.9e-26;
Matches 69; Conservative 35; Mismatches 54; Indels 5; Gaps 1;

OY 11 WMLSLMFLSWVEGEESQKLPSSRTCPGSGVAYGSCYSLILIPOTWMAELSCOMH 70
DB 7 FTLISCLVLPSPQGEARLPSPKISCPBSNAYSSCYTFEDRLTMADADLPFCOM 66
OY 71 FSGHLAFLISTGEITFVSSLVNLSLTAYQYIMIGLHDPSSHGLPNSGGMKSSNVLTFT 130
DB 67 NSGYLVSVLSQAEQNFVSLIKESCTDANVTGTHDPK-----RNRMHWSGSLFLYK 121
OY 131 NWRNPSTIADRGCAVLSQKSGFQKWRDFNCENELPYICKFK 173

Db 122 SWATGSPNNSNRGYCVSLTSMYGRKKWKDKDCAQYSFYCKFK 164

Search completed: April 16, 2003, 10:46:44
Job time : 14 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:43:30 ; Search time 32 Seconds
(without alignments)
1120.381 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 958
Sequence: 1 MPMPTLCMSMLSLCMFL.....QKWRDNCENELPYCKFKV 174

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mmc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	78.3	138	11	09QYF7 mesocricetu
2	676	70.6	175	11	09JMH1 09JMH1 mus muscu
3	676	70.6	175	11	09QUS9 09QUS9 mus muscu
4	437	45.6	146	11	09CVF4 09CVF4 mus muscu
5	360	37.6	98	11	09QYF8 09QYF8 mus muscu
6	277	28.9	86	11	09COB4 09COB4 mus muscu
7	246.5	25.7	157	11	09DBS8 09DBS8 mus muscu
8	244.5	25.5	157	11	09DBS5 09DBS5 mus muscu
9	196	20.5	152	13	09DG39 09DG39 agkistrodon
10	194	20.3	158	13	09QW17 09QW17 bungarus fa
11	191	19.9	158	13	08UNC6 08UNC6 agkistrodon
12	190	19.8	152	13	09IAM1 09IAM1 agkistrodon
13	190	19.8	158	4	09BYZ8 09BYZ8 homo sapien
14	184	19.2	158	13	09OW18 09OW18 bungarus fa
15	184	19.2	158	13	09OW16 09OW16 bungarus mu
16	183	19.1	146	13	09DEF8 09DEF8 agkistrodon

17	182	19.0	152	13	09DEF9 09DEF9 agkistrodon
18	180	18.8	146	13	09DC31 09DC31 agkistrodon
19	179	18.7	146	13	09IAM0 09IAM0 agkistrodon
20	178	18.6	146	13	09I840 09I840 agkistrodon
21	176	18.4	146	13	09BUU0 09BUU0 trimeresu
22	172	18.0	134	5	09XYX3 09XYX3 hydra magni
23	171.5	17.9	136	13	09I841 09I841 agkistrodon
24	171	17.8	124	13	09BSM5 09BSM5 agkistrodon
25	169	17.6	134	5	09UB05 09UB05 hydra atten
26	169	17.6	134	5	025199 025199 hydra atten
27	168.5	17.6	135	13	09PSM4 09PSM4 laecheis mu
28	168	17.5	134	5	09XYX2 09XYX2 hydra atten
29	166.5	17.4	145	13	09YGN4 09YGN4 agkistrodon
30	166	17.3	134	5	09XYX4 09XYX4 hydra Olig
31	166	17.3	154	13	09YGN5 09YGN5 agkistrodon
32	165.5	17.3	157	13	09YGN9 09YGN9 agkistrodon
33	164.5	17.2	2109	13	P79787 09YGN9 agkistrodon
34	162	16.9	148	13	093427 093427 gallus gall
35	162	16.9	1722	4	075913 075913 crotales du
36	161.5	16.9	155	13	09DER2 09DER2 homo sapien
37	161	16.8	1722	4	060449 060449 homo sapien
38	160	16.7	166	13	09OWJ8 09OWJ8 homo sapien
39	158.5	16.5	315	4	09UPK6 09UPK6 homo sapien
40	158.5	16.5	1321	4	014594 014594 homo sapien
41	158.5	16.5	1723	11	060767 060767 mus muscu
42	158.5	16.5	1723	11	091X18 091X18 mus muscu
43	157	16.4	1479	11	064449 064449 mus muscu
44	156.5	16.3	1487	11	062028 062028 mus muscu
45	156	16.3	1326	4	Q13019 Q13019 homo sapien

ALIGNMENTS

RESULT 1
ID 09QYF7 PRELIMINARY: PRT: 138 AA.
AC 09QYF7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Islet neogenesis associated protein (Fragment).
GN INGAP.
OS Mesocricetus auratus (golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nara K., Akiyama T., Shervani N.J., Kobayashi S.,
Tomiloka-Kumagai T., Ito S., Takasawa S., Okamoto H.,
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
of all three types of Reg family gene in a 75 kilobase mouse genomic
region.";
RT Gene 246:111-122(2000).
RL EMBL: AB035211; BA88566.1; -
DR HSSP: P05451; IOPD.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
FT NON_TER
SQ SEQUENCE 138 AA: 15565 MW: 453888AADI8524 CRC64;
Query Match 78.3%; Score 750; DB 11; Length 138;
Best Local Similarity 98.6%; Pred. NO. 5.4e-67;
Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 37 ITCPQGSVAVGYSYSLIITPQTSNALS COMHPSGHIAFLSTGTEFFVSLVKSLT 96

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Db 1 ITCPQSGVAVAGSYCYSLILIPQWNSNAELSCQMHPSCHLAFLLSTGRTTFFVSSILVKNLSLT 60
QY 97 AYQYTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGYCAVLISQKSGFQK 156
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 AYQYTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGYCAVLISQKSGFQK 120
QY 157 WRDNCENELPYICKFKV 174
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 WRDNCENELPYICKFKV 138

RESULT 2
09JUN1 PRELIMINARY: PRT: 175 AA.
ID 09JUN1
AC 09JUN1
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE INGP related protein.
GN INGP OR INGPAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BDF-1; TISSUE-DUODENUM;
RX MEDLINE=20033449; PubMed=10564727;
RA Sasahara K., Yamoka T., Moritani M., Yoshimoto K., Kuroda Y.,
  Itakura M.;
RT "Molecular cloning and tissue-specific expression of a new member of
  the regenerating protein family, Islet neogenesis-associated protein-
  related protein.";
RL Biochim. Biophys. Acta 1500:142-146(2000).
DR EMBL; AB028625; BAA92141.1; -
DR HSSP; P05451; IQDD.
DR MGD; MGI:1353426; Ingapp.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c_1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 175 AA; 20021 MW; 0A92FA6112BC6B53 CRC64;

Query Match 70.6%; Score 676; DB 11; Length 175;
Best Local Similarity 72.2%; Pred. No. 1.6e-59;
Matches 122; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 5 TLRMSMMLSCIMPLSWVEGESQKRLPSSRTCPQSGVAVAGSYCYSLILIPQWNSNAE 64
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 6 TLHSMNMMLCCIMLSWVGESQKRLSPRISCPQEAQVAGSYCYLLILEPQWANE 65
QY 65 LSCQMHPSCHLAFLLSTGRTTFFVSSILVKNLSLTAYQYTWGLDPSHGTPNGSGWKNSS 124
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 66 IHCQKHFSGHLAFLLTYGRTTFFVSSILVKNLSLTFFPYTWGLDPSHGTPNGSGWKNSS 125
QY 125 NVLTFYNERNPSIADRGYCAVLISQKSGFQKWRDNCENELPYICKFK 173
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 126 DPLTFYTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGYCAVLISQKSGFQK 174

RESULT 3
09JUN1 PRELIMINARY: PRT: 175 AA.
ID 09JUN1
AC 09JUN1
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE REG III delta precursor (Islet neogenesis associated protein-related
  protein).
GN INGPAP OR REG3D.
OS Mus musculus (Mouse).

```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Abe M., Nata K., Tomioka-Kumagai T., Takasawa S., Ito S., Okamoto H.;
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
  of all three types of Reg family genes in 75-kilobase mouse genomic
  region.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
  Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
  Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamane I.,
  Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schirrl L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
  Blake J., Botfield D., Boyle N., Carninci P., de Bonaldo M.F.,
  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamli M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
  Nordone P., Ring B., Schoenbach M., Rodriguez I., Sakamoto T.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Winkler L.,
  Wyszewski H., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
  Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AB035204; BAA88564.1; -
DR EMBL; AB035205; BAA88565.1; -
DR EMBL; AK019033; BAB31518.1; -
DR HSSP; P05451; IQDD.
DR MGD; MGI:1353426; Ingapp.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatins_ac.
DR Pfam; PF00059; lectin_c_1.
DR PRINTS; PR01504; PNCREATITSAF.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW SIGNAL.
SQ SEQUENCE 175 AA; 20037 MW; 0A88D67512BC6B53 CRC64;

Query Match 70.6%; Score 676; DB 11; Length 175;
Best Local Similarity 72.2%; Pred. No. 1.6e-59;
Matches 122; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 5 TLRMSMMLSCIMPLSWVEGESQKRLPSSRTCPQSGVAVAGSYCYSLILIPQWNSNAE 64
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 6 TLHSMNMMLCCIMLSWVGESQKRLSPRISCPQEAQVAGSYCYLLILEPQWANE 65
QY 65 LSCQMHPSCHLAFLLSTGRTTFFVSSILVKNLSLTAYQYTWGLDPSHGTPNGSGWKNSS 124
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 66 IHCQKHFSGHLAFLLTYGRTTFFVSSILVKNLSLTFFPYTWGLDPSHGTPNGSGWKNSS 125
QY 125 NVLTFYNERNPSIADRGYCAVLISQKSGFQKWRDNCENELPYICKFK 173
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 126 DPLTFYTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGYCAVLISQKSGFQK 174

RESULT 4
09JUN1 PRELIMINARY: PRT: 146 AA.
ID 09JUN1
AC 09JUN1
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

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DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Rat generating islet-derived, mouse homolog 3 alpha (Fragment).
GN REG3A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK008470; BAB25687.1;
DR HSSP: P03451; 10DD.
DR MGD: MGI:109408; Reg3a.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
FT NON_TER
SQ SEQUENCE 146 AA; 16161 MW; 76D73B81BEC5FB1 CRC64;

Query Match 45.6%; Score 437; DB 11; Length 146;
Best Local Similarity 51.0%; Pred. No. 7.8e-36;
Matches 74; Conservative 28; Mismatches 43; Indels 0; Gaps 0;

QY 29 QKLPSSRLTCEPGSVAYGSCYSLILIPQVSNMELSCOMHFSCHLAFLLSTGEITPVS 88
DB 1 EKEVPSPTSCPMGYKARYSHSYALVMPKSWFQADLVCOQKRPSSGLVLSLGGFASPV 60
QY 89 SLVKNSTLTAQYIMIGLHPSPHGTLPNGSGMKWSSNVLTFFNERNRSIADNGYCAVL 148
DB 61 SLVNGRDYVQDITWIGLHPTMGQPNCGMGWMSNDVLTNLMDGDPSTVYNGHCSL 120
QY 149 SQRSGFQKWRDFNCENELPYICKFK 173
DB 121 TASGGFLKMGDYCDGLTDFVCKFK 145

RESULT 5
O9QYF8 PRELIMINARY; PRT; 98 AA.
AC O9QYF8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Reg III delta (Fragment).
GN INGPAPR OR REG3A OR REG3D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]

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RP SEQUENCE FROM N.A.
RA MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nata K., Akiyama T., Shervani N.J., Kobayashi S.,
RA Tomioka-Kumagai T., Ito S., Takasawa S., Okamoto H.;
RT Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region.";
RL Gene 246:111-122(2000).
DR EMBL: AB035203; BAB8562.1;
DR HSSP: P03451; 1LIT.
DR MGD: MGI:109408; Reg3a.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
FT NON_TER
SQ SEQUENCE 98 AA; 11248 MW; 871ECC93FAD00595 CRC64;

Query Match 37.6%; Score 360; DB 11; Length 98;
Best Local Similarity 69.9%; Pred. No. 2.2e-28;
Matches 72; Conservative 7; Mismatches 14; Indels 10; Gaps 2;

QY 5 TCRSMMLSCIMPLSVWEGEESQKLPSSRLTCEPGSVAYGSCYSLILIPQVSNM 64
DB 6 TLHSMWML-C-----EQQKRLSPRISCPQEAQYSCYLLILPQTANNE 55
QY 65 LSCQMFHSHLAFLLSTGEITPVSILVKNSTLTAQYIMIGLHD 107
DB 56 IHCQKHFHSHLAFLLTYELIFVSLVKNSTLTPFYIMIGLHD 98

RESULT 6
O9QCE4 PRELIMINARY; PRT; 86 AA.
AC O9QCE4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rat generating islet-derived, mouse homolog 3 alpha (Fragment).
GN REG3A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK008140; BAB25488.1;
DR EMBL: AK008050; BAB25430.1;
DR HSSP: P03451; 10DD.
DR MGD: MGI:109408; Reg3a.
DR InterPro: IPR001304; Lectin_C.

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DR pfam: PF00059: lectin_c.1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE: PS00411; C_TYPE_LLECTIN_2; 1.
 FT NON-TER 1 1

SO SEQUENCE 86 AA; 9575 MW; 98088079FC357EB CRC64;

Query Match 28.9%; Score 277; DB 11; Length 86;
 Best Local Similarity 52.9%; Pred. No. 3.5e-20;
 Matches 45; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

OY 89 SLVKNSLTAYQYTWIGLHDPSSGHTLPNGSGKMWSSNVLTFTYWRNPSTADRGCAVL 148
 DB 1 SLVNGRVNDQDIDWIGLHDPPTMGQOPNGGGMWMSNDVLTNTMDGDPSTYVNRGCGSL 60

OY 149 SOKSGFQKWDPNCENELPYICKER 173
 DB 61 TASSGFLKMGDYCCDGLTFVCKEK 85

RESULT 7
 OY0858 PRELIMINARY: PRT; 157 AA.

AC Q9D858;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 2010002L15RIK protein.
 GN 2010002L15RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RL EMBL: AK008438; BAB25669.1;
 DR HSSP: P05451; 1QDD.
 DR MGD: MGI:1914959; 2010002L15RIK.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SO SEQUENCE 157 AA; 18474 MW; FD96F36CFB989368 CRC64;

Query Match 25.7%; Score 246.5; DB 11; Length 157;
 Best Local Similarity 32.5%; Pred. No. 7.5e-17;
 Matches 55; Conservative 30; Mismatches 67; Indels 17; Gaps 6;

OY 9 MSMLLSCLMFLSWBEGESQKRLPSRRITCPGGSVAAGSYCYSLILPQWTSNALSQ 68
 DB 1 MAVKGVALLILSLWAGPEVLSDI--LRPSCAPGWFFYRSHCYGYFRKLRNMSHALEBCQ 58

OY 69 MHRSSG-HLAFLSTGEITFVSSLVKNSLTAYQ---TWIGLHDPSSGHTLPNGSGKMWSS 124
 DB 59 STNGSHSLASVINOKE----ASVSKYITIGYRNLPMWIGLHDPQKQL-----WQWTDG 109

OY 125 NVLTFTYWRNPSTADRGCAVLISQKSGFQKWDPNCENELPYICKER 173
 DB 110 STNLYRRW--NPRTKSEARHCAEMNPDKFLTWKNGCANRQHFLCKYK 156

RESULT 8
 OY08G5 PRELIMINARY: PRT; 157 AA.

AC Q9D8G5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 2010002L15RIK protein (RIKEN cDNA 2010002L15 gene).
 GN 2010002L15RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RL EMBL: AK008049; BAB25429.1;
 DR HSSP: P05451; 1QDD.
 DR MGD: MGI:1914959; 2010002L15RIK.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SO SEQUENCE 157 AA; 18398 MW; F3981722BBD83968 CRC64;

Query Match 25.5%; Score 244.5; DB 11; Length 157;
 Best Local Similarity 33.5%; Pred. No. 1.2e-16;
 Matches 54; Conservative 27; Mismatches 63; Indels 17; Gaps 6;

OY 17 IMFLSWBEGESQKRLPSRRITCPGGSVAAGSYCYSLILPQWTSNALSQMFSS-HL 75
 DB 9 LLISLVNAPVYLSDI--LRPSCAPGWFFYRSHCYGYFRKLRNMSHALEBCQSGNSHL 66

OY 76 AFLISTGEITFVSSLVKNSLTAYQ---TWIGLHDPSSGHTLPNGSGKMWSSNVLTFTY 132
 DB 67 ASVLINOKE----ASVSKYITIGYRNLPMWIGLHDPQKQL-----WQWTDGSTNLYRRW 117

QY 133 ERNESTIADRGCAVLSQSGFQKWDENCENELPYCKEK 173
 DB 118 -NPRTESEARHCAMENPKDKFTLWKNKNCANROHFLCKYK 156

RESULT 9

Q9DG39 PRELIMINARY; PRT: 152 AA.

AC Q9DG39; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DE 01-MAR-2001 (Tremblrel. 19, last annotation update)
 GN Halysin A-chain precursor.

OS Agkistrodon halys pallasi (Chinese water moccasin) (Gloydius halys pallasi).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Gloydius.
 NC NCBI_TaxID=8714;
 RN [1]

SEQUENCE FROM N.A.

RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
 RT "A novel coagulation factor Xa inhibitor from Korean snake
 (Agkistrodon halys) venom." to the EMBL/GenBank/DBJ databases.

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF190827; AAG17178.1; -.
 DR HSSP; P23806; 11xx.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Signal.

FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 152 HALYXIN A-CHAIN.
 SQ SEQUENCE 152 AA; 17455 MW; BD074D1DC280C28D CRC64;

Query Match 20.5%; Score 196; DB 13; Length 152;
 Best Local Similarity 30.3%; Pred. No. 7.7e-12;
 Matches 50; Conservative 32; Mismatches 61; Indels 22; Gaps 7;

QY 9 MSWMLSCMFLMVGSEBQKLPSSRTICPGGSVAAGSYCYSLILIPQWNSNAELSC 68
 DB 7 LSEFL--VFLS-----LSGTGADCSGMSSTEGHCYNFHLFKTMAERPCR 54
 QY 69 MPEFG-HLAPLSTGETTFVSSLVKNSLAYO-YIMIGLHDSHGLTPNGSGKWSNV 126
 DB 55 KOVGAHLVIESSEEDAFVQALVSENMKRYGIYIWIGLR--VRGKKKCCS-QMSDSS 111
 QY 127 LTFNWERNPISIAADRGCAVLSQSGFQKWDENCENELPYCK 171
 DB 112 VSYGNW-----IEASTKICLGLOKTEFRKWNITYGGENPVCE 151

RESULT 10

Q90W17 PRELIMINARY; PRT: 158 AA.

AC Q90W17; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE 01-MAR-2002 (Tremblrel. 20, last annotation update)
 GN C-type lectin-like protein 2.

OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 NC NCBI_TaxID=8613;
 RN [1]

SEQUENCE FROM N.A.

RA Zha H.-G., Zhang Y.;
 RT "CDNA cloning and characterization of C-type lectin-like proteins from

RT Elapidae snakes." to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF354271; AAK43585.1; -.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Lectin.

SQ SEQUENCE 158 AA; 18254 MW; 5F0218970DA17453 CRC64;

Query Match 20.3%; Score 194; DB 13; Length 158;
 Best Local Similarity 29.6%; Pred. No. 1.3e-11;
 Matches 48; Conservative 28; Mismatches 68; Indels 18; Gaps 6;

QY 16 CL--FELSWVEEBEQKLPSSRTICPGGSVAAGSYCYSLILIPQWNSNAELSCMHESG 73
 DB 10 CLTAMFLS-LSGAEC-----YTCPIDWLPKNGLCYKFSNPKSWLDAEMFCRKRFG 60
 QY 74 -HLAPLSTGETTFVSSLVKNSLAYOYIMIGLHDSHGLTPNGSGKWSNVLTFFNM 132
 DB 61 CHLASIHRRDADSLAEVSDYLDKDDGNVWIGLNDPQ-----KKRTWVMSDRSSNYFEM 115

QY 133 ER-NESTIADRGCAVLSQSGFQKWDENCENELPYCKEK 173
 DB 116 NQEPFNSKNEYCYHMAPTGYLKMNDAPCETLHPYCKCK 157

RESULT 11

Q8UYC6 PRELIMINARY; PRT: 158 AA.

AC Q8UYC6; 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
 GN Antichrombin 1 A chain.

OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 NC NCBI_TaxID=36307;
 RN [1]

SEQUENCE FROM N.A.

RA Yu H., Xiang K., Liu J.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF463522; AAL6391.1; -.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

SQ SEQUENCE 158 AA; 17950 MW; A73AC895997BFD7 CRC64;

Query Match 19.9%; Score 191; DB 13; Length 158;
 Best Local Similarity 30.7%; Pred. No. 2.5e-11;
 Matches 43; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 39 CPQGSVAAGSYCYSLILIPQWNSNAELSC-OMHESGHLAPLSTGETTFVSSLVKNSLA 97
 DB 27 CPFGMSAYDQCYGYIKPKKNMDDAERCFQAGGHLVIESGGERDFVQALVSGSIS 86
 QY 98 YQ-YIMIGLHDSHGLTPNGSGKWSNVLTFFN-----WERNPSTIADRGCAVLSQGS 152
 DB 87 VEDHWVTGILRVONK--EKQSTFMSDSSVSVENLLELYMRK-----CGALERET 134

RESULT 12

Q91AM1 PRELIMINARY; PRT: 152 AA.

AC Q91AM1; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Agkistrodon A chain.
 OS Agkistrodon acutus (Hundred-pace snake) (Delnagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Delnagkistrodon.
 NC NCBITaxID=36307;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM;
 RA Yu H.-X., Xiang K.-J., Liu J.,
 RT *cDNA sequencing and analysis of eleven C-type lectin-like protein
 RT subunits from Agkistrodon acutus.";
 RT Chin. J. Biochem. Biophys. 0:0-0(2002).
 DR EMBL: AF176420; AAF26286.2; -; 76A0F636BFD07AB CRC64;
 SQ SEQUENCE 152 AA; 17109 MW; 76A0F636BFD07AB CRC64;

Query Match 19.8%; Score 190; DB 13; Length 152;
 Best Local Similarity 27.4%; Pred. No. 3e-11;
 Matches 43; Conservative 32; Mismatches 62; Indels 20; Gaps 5;

QY 17 LMFSLVVEEESQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFS-GHL 75
 DB 13 VYFLS-----LSGTADCCSSGMSYEGHCYKVKOSKRTDASEFCTKQVNGHL 62
 QY 76 AFLSTGEITFYVSLVKNLSL-TAYQYIWIGLHPSHGTLPNGSGMKWSSNVLTFFYMW 134
 DB 63 VSIESSEGEAFYVGLIAOKIKSAKIHVIGLMAQNK--EKQCSIESDGSISSEYMW-- 117
 QY 135 NPSTADRGCAVLISOKSGFQKWRDPCNCELPYICK 171
 DB 118 ---IEESKCKLGVHETGFKMENFYCEQDPFYCE 151

RESULT 13

Q9BYZ8

PRELIMINARY; PRT; 158 AA.

ID Q9BYZ8
 AC Q9BYZ8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Regenerating gene type IV (Regenerating gene type IV precursor)
 DE (Gastrointestinal secretory protein GISP).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBITaxID=9606;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=21210973; PubMed=11311942;
 RA Hartup J.C., Zhang H., Bonaldo M.F., Soares M.B., Dieckgraefe B.K.;
 RT Isolation and characterization of a cDNA encoding a novel member of
 RT the human regenerating protein family: Reg IV(1)."
 RL Biochim. Biophys. Acta 1518:287-293(2001).
 RN- [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=COLON CANCER;
 RA Violette S., Fesler E., Dussaux E., Citadelle D., Chamaz J.,
 RT lacasa M., Lesuffleur T.;
 RT "The new intestinal Reg IV gene is involved in drug-resistance of
 RT colon tumor cells.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN- [3]
 RP SEQUENCE FROM N.A.
 RP TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN- [4]
 RP SEQUENCE FROM N.A.
 RP Lin W.-C.;
 RT "Identification of gastrointestinal secretory protein (GISP), a new

RT member of lithostathine gene family.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007243; AAG02562.1; -;
 DR EMBL: AF345934; AAK59869.1; -;
 DR EMBL: BC017089; AAH17089.1; -;
 DR EMBL: AF254415; AAK48435.1; -;
 DR HSSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin C.
 DR InterPro: IPR003990; Pancreatis_ac.
 DR Pfam: PF00059; Lectin_C; 1.
 DR PRINTS: PRO1504; PROKATITAP.
 DR SMART: SM0034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 RT Signal.
 FT SIGNAL.
 SQ SEQUENCE 158 AA; 18230 MW; 7308849CBBDE93E CRC64;

Query Match 19.8%; Score 190; DB 4; Length 158;
 Best Local Similarity 30.1%; Pred. No. 3.2e-11;
 Matches 50; Conservative 28; Mismatches 66; Indels 22; Gaps 8;

QY 12 MLTSLMFSLVVEEESQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFS 71
 DB 10 LLSGLA-KTGVLDIIL-----RPSGAPGWFYHKNGCYGRKLRLNNSDALLDQSYG 62
 QY 72 SG-HLAFSLTGEITFYVSLVKNLSL-TAYQYIWIGLHPSHGTLPNGSGMKWSSNVLT 127
 DB 63 NHAHLASTLSKE---ASTIAEYISGQKSPWILHDPQ-----KROQWQWIDGAMT 113
 QY 128 PFYMERNPSTADRGCAVLISOKSGFQKWRDPCNCELPYICK 173
 DB 114 LYRSMN-GKSMGKN-HCAEMSSNNFLTWSNCCNKRQHFLLKYR 157

RESULT 14

Q90W18

PRELIMINARY; PRT; 158 AA.

ID Q90W18
 AC Q90W18;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-type lectin-like protein 1.
 OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NC NCBITaxID=8613;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=VENOM GLAND;
 RA Zha H.-G., Zhang Y.;
 RT "cDNA cloning and characterization of C-type lectin-like proteins from
 RT Elapidae snakes.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF354270; AAK43584.1; -;
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; Lectin_C; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 RT Signal.
 SQ SEQUENCE 158 AA; 18638 MW; ECF8593FMA182B8 CRC64;

Query Match 19.2%; Score 184; DB 13; Length 158;
 Best Local Similarity 28.4%; Pred. No. 1.2e-10;
 Matches 46; Conservative 27; Mismatches 71; Indels 18; Gaps 6;

QY 16 CL--MFSLVVEEESQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFS 73
 DB 10 CLIAFLS-LSAEC-----YTCPIDWLPKNGCLTKYPSKRTYFDAMCRKFKRG 60
 QY 74 -HLAFSLTGEITFYVSLVKNLSL-TAYQYIWIGLHPSHGTLPNGSGMKWSSNVLTFFYMW 132
 DB 63 NHAHLASTLSKE---ASTIAEYISGQKSPWILHDPQ-----KROQWQWIDGAMT 113

Db 61 CHLASLHSDADAVSESEYISDYITGGHWIGIRDTKKYI-----WETDRSRDPLPW 115
QY 133 -ERNPSTADRGYCAVLISOKSGFQKWRDPNCENELPYICKER 173
Db 116 RKKOPDHFNNEFCVEIVNFTGYLQWMDNCALRPFLCQCK 157

RESULT 15

Q90W16 PRELIMINARY; PRT; 158 AA.
AC Q90W16;
DT 01-DEC-2001 (TREMBLrel, 19, Created)
DT 01-DEC-2001 (TREMBLrel, 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel, 20, last annotation update)
DE C-type lectin-like protein 1.
OS Bungarus multiclincus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_taxid=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Zha H.-G., Zhang Y.;
RT "cDNA cloning and characterization of C-type lectin-like proteins from
Elapidae snakes".
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF354272; AAK43586.1; -.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_c; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 158 AA; 18706 MW; 66B71A29D104805 CRC64;

Query Match 19.2%; Score 184; DB 13; Length 158;
Best Local Similarity 29.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 25; Mismatches 72; Indels 18; Gaps 6;

QY 16 CL-MFLSWVEGESQKLPSSRITCPQGSVAYGSYCSLLIPQWTSNAELSCOMHFSG 73
Db 10 CLAMFLS-LRGAEC-----YTCPIDWLPKNGLCYVFSGHKHTWFDAEKCYCKRFRG 60
QY 74 -HLAFLSTGEITFVSSLVNASTAYQIYIWIGLHDSHTLPNGSGMKWSSNVLTFTNW 132
Db 61 CHLASLHSDADAVSESEYISDYITGGHWIGIRDTKKYI-----WETDRSRDPLPW 115
QY 133 ERN-PSIADRGYCAVLISOKSGFQKWRDPNCENELPYICKER 173
Db 116 RKNQPDHFNNEFCVEIVNFTGYLQWMDNCALRPFLCQCK 157

Search completed: April 16, 2003, 10:47:23
Job time : 34 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:45:50 ; Search time 28 Seconds
(without alignments)

182.842 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 958
Sequence: 1 MLPMTLCRMSMMLSCIMFL.....QKWRDNCENELPYCKEKV 174

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-NA: *
1: /cgn2.6/ptodata/1/1aa/5A-COMB.pep: *
2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep: *
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep: *
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep: *
5: /cgn2.6/ptodata/1/1aa/PTUS-COMB.pep: *
6: /cgn2.6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958	100.0	174	2	US-08-401-530A-2
2	958	100.0	174	2	US-08-709-662-2
3	958	100.0	175	1	US-08-909-725-6
4	598	62.4	175	2	US-08-401-530A-3
5	598	62.4	175	2	US-08-709-662-3
6	572	59.7	175	2	US-08-464-637-2
7	572	59.7	175	2	US-08-401-530A-4
8	572	59.7	175	2	US-08-709-662-4
9	572	59.7	175	2	US-08-822-261-3
10	566	59.1	174	1	US-07-778-156-7
11	566	59.1	174	2	US-08-822-261-4
12	566	59.1	174	2	US-08-422-166-7
13	557	58.1	175	2	US-08-822-261-1
14	557	58.1	184	1	US-07-778-156-2
15	557	58.1	184	1	US-08-422-166-2
16	518	54.1	174	2	US-08-401-530A-5
17	518	54.1	174	2	US-08-709-662-5
18	464	50.5	158	1	US-07-778-156-3
19	464	50.5	158	2	US-08-422-166-3
20	466	48.6	174	2	US-08-401-530A-6
21	466	48.6	174	2	US-08-709-662-6
22	402.5	42.0	166	2	US-08-729-103-4
23	395.5	41.3	165	2	US-08-401-530A-7
24	395.5	41.3	165	2	US-08-729-103-3
25	395.5	41.3	165	2	US-08-709-662-7
26	257.5	20.1	117	6	5514562-15
27	193	20.1	134	1	US-07-893-929A-2

28	193	20.1	134	5	PCT-US92-10344-2	Sequence 2, Appl1
29	190	19.8	158	2	US-08-729-103-1	Sequence 1, Appl1
30	190	19.8	158	2	US-08-468-413-2	Sequence 2, Appl1
31	190	19.8	158	3	US-09-162-508-2	Sequence 2, Appl1
32	190	19.8	158	3	PCT-US95-07169-2	Sequence 2, Appl1
33	185	19.3	131	1	US-07-893-929A-1	Sequence 1, Appl1
34	185	19.3	131	5	PCT-US92-10344-1	Sequence 1, Appl1
35	172	18.0	130	1	US-07-893-929A-7	Sequence 7, Appl1
36	172	18.0	133	1	PCT-US92-10344-7	Sequence 7, Appl1
37	172	18.0	133	1	US-07-893-929A-9	Sequence 9, Appl1
38	172	18.0	133	5	PCT-US92-10344-9	Sequence 9, Appl1
39	164	17.1	125	1	US-07-893-929A-3	Sequence 3, Appl1
40	164	17.1	125	5	PCT-US92-10344-3	Sequence 3, Appl1
41	162	16.9	132	1	US-07-893-929A-5	Sequence 5, Appl1
42	162	16.9	132	5	PCT-US92-10344-5	Sequence 5, Appl1
43	161	16.8	172	4	US-09-194-612A-1	Sequence 1, Appl1
44	160	16.7	123	1	US-07-893-929A-4	Sequence 4, Appl1
45	160	16.7	123	5	PCT-US92-10344-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-401-530A-2
Sequence 2, Application US/08401530A
Patent No. 5834590.

GENERAL INFORMATION:

APPLICANT: Vitnik, Aaron I.
APPLICANT: Piltenger, Gary L.
APPLICANT: Rataeloff, Ronit
APPLICANT: Rosenbergl, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A. 32,141
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-401-530A-2

Query Match 100.0%; Score 958; DB 2; Length 174;
Best local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPMTLCRMSMMLSCIMFLSWVGESQKKRPSRTCTQGSVAAGSYSLILPQW 60
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Db 1 MLPTLCRSMWMLSCIMFLSWVEGESQKLPSSRTCPGSAVAGSYCSLLIPQTM 60
QY 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
QY 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 174
Db 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 174

RESULT 2

US-08-709-662-2
; Sequence 2, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: ISLET PROTEIN INVOLVED IN PANCREATIC
; TITLE OF INVENTION: ISLET NEOGENESIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/709,662
; APPLICATION NUMBER: US/08/709,662
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 00570,59178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-662-2

Query Match 100.0%; Score 958; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2,7e-98;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
QY 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 174
Db 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 174

RESULT 3

US-08-909-725-6
; Sequence 6, Application US/08909725
; Patent No. 5804421
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Pittenger, Gary
; APPLICANT: Rafaeloff-Phall, Ronit
; APPLICANT: Barlow, Scott
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
; TITLE OF INVENTION: INCAP IN BACTERIAL AND EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,725
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,096
; FILING DATE: 30-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,145
; REFERENCE/DOCKET NUMBER: 0570,05173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 97430 BMB UT
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-909-725-6

Query Match 100.0%; Score 958; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 2,8e-98;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCRSMWMLSCIMFLSWVEGESQKLPSSRTCPGSAVAGSYCSLLIPQTM 60
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QY 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLILSTGEITFVSSLVKNLSLTAYQYTWIGLHDPSSHGLTPNGSGWK 120
QY 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 174
Db 121 WSSSNVLTFFYNERNPSTIADRGCAVLSQKSGFQKMRDPCENELPYICKFKY 175

RESULT 4
US-08-401-530A-3
; Sequence 3, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence

US-08-401-530A-3


```

; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; TITLE OF INVENTION: ISLET NEOGENESIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,530A
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 00570.48743
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; US-08-401-530A-3

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Query Match 62.4%; Score 598; DB 2; Length 175;
Best Local Similarity 61.6%; Pred. No. 1.8e-58;
Matches 101; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

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QY 9 MSMLLSCLMTLSWVEGSEOKLPSRITCPGSAVAGSYCYSLILIPQWNAELSCQ 68
DB 10 MSMLLSCLMTLSQVQGEDSPKIPSAISCPKSGQATGSCYALPQIPWDAELACQ 69
QY 69 MFSGHLAFLSTGETFEVSSLVKNSLTAYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 128
DB 70 KREGHIVSYLVNVAEASFLASMKNTGNSYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 129
QY 129 FYWNERNPSTADRGYCAVLISOKSGFQKWRDNCENELPYICKE 172
DB 130 YVWNERNPSTADRGYCAVLISOKSGFQKWRDNCENELPYICKE 173

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RESULT 5
US-08-709-662-3
; Sequence 3, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Piltenger, Gary L.
; APPLICANT: Ratajecki, Ronald
; APPLICANT: Rosendberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; TITLE OF INVENTION: ISLET NEOGENESIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.

```

```

; COUNTRY: US
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,662
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 00570.59178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; US-08-709-662-3

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Query Match 62.4%; Score 598; DB 2; Length 175;
Best Local Similarity 61.6%; Pred. No. 1.8e-58;
Matches 101; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

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QY 9 MSMLLSCLMTLSWVEGSEOKLPSRITCPGSAVAGSYCYSLILIPQWNAELSCQ 68
DB 10 MSMLLSCLMTLSQVQGEDSPKIPSAISCPKSGQATGSCYALPQIPWDAELACQ 69
QY 69 MFSGHLAFLSTGETFEVSSLVKNSLTAYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 128
DB 70 KREGHIVSYLVNVAEASFLASMKNTGNSYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 129
QY 129 FYWNERNPSTADRGYCAVLISOKSGFQKWRDNCENELPYICKE 172
DB 130 YVWNERNPSTADRGYCAVLISOKSGFQKWRDNCENELPYICKE 173

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RESULT 6
US-08-464-637-2
; Sequence 2, Application US/08464637
; Patent No. 5834214
; GENERAL INFORMATION:
; APPLICANT: Iovanna, Juan-Luicio
; APPLICANT: Dagorn, Jean-Charles
; APPLICANT: Keim, Volker
; APPLICANT: Saries, Jacques
; TITLE OF INVENTION: Detection of Pancreatitis-Associated
; TITLE OF INVENTION: Protein for Diagnosis of Cystic Fibrosis or Pancreatic
; TITLE OF INVENTION: Disease (as amended).
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-3487
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,637

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FILED DATE: 30-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 2121-107P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-637-2

Query Match 59.7%; Score 572; DB 2; Length 175;
Best Local Similarity 57.6%; Pred. No. 1,4e-55;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTICRMSNMLLSCLMTLSWVEGESQKKLPSSRITCPQGSVAVGYCYSLILIPQWNS 62
DB 4 PMALPSVSMMLSCMLTSLQVGEPEQRELPARIRCPKSGKAVGSHCYALFLSPKSWTD 63
QY 63 AELSCOMHPSGHLAFLSTGCTFPVSSLYKNSLTAYQYIWIIGLHDPHSGTLPNGSGMKNS 122
DB 64 ADLACOKRPSGNLYSLGAEGSFVSLVKSIGNSYTWIGLHDPGTGTEPNGBEWMNS 123
QY 123 SSNVLFYTWERNPSTIAADRGICAVLSQSGFQKWRDPCNENELPYCKF 172
DB 124 SSDVMNYFAMERNPSTISSPGHCASLSRSTAFLEMKDYNCNVRLPYCKF 173

RESULT 7
US-08-401-530A-4
Sequence 4, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
APPLICANT: Vink, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570,48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9299
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-401-530A-4

Query Match 59.7%; Score 572; DB 2; Length 175;
Best Local Similarity 57.6%; Pred. No. 1,4e-55;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTICRMSNMMLSCMLTSLWVEGESQKKLPSSRITCPQGSVAVGYCYSLILIPQWNS 62
DB 4 PMALPSVSMMLSCMLTSLQVGEPEQRELPARIRCPKSGKAVGSHCYALFLSPKSWTD 63
QY 63 AELSCOMHPSGHLAFLSTGCTFPVSSLYKNSLTAYQYIWIIGLHDPHSGTLPNGSGMKNS 122
DB 64 ADLACOKRPSGNLYSLGAEGSFVSLVKSIGNSYTWIGLHDPGTGTEPNGBEWMNS 123
QY 123 SSNVLFYTWERNPSTIAADRGICAVLSQSGFQKWRDPCNENELPYCKF 172
DB 124 SSDVMNYFAMERNPSTISSPGHCASLSRSTAFLEMKDYNCNVRLPYCKF 173

RESULT 8
US-08-709-662-4
Sequence 4, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vink, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570,59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-709-662-4

Query Match 59.7%; Score 572; DB 2; Length 175;
Best Local Similarity 57.6%; Pred. No. 1,4e-55;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

Patent No. 5935813
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 189601
US-08-822-261-4
Query Match 59.1%; Score 566; DB 2; Length 174;
Best Local Similarity 57.4%; Pred. No. 6.3e-55;
Matches 97; Conservative 34; Mismatches 38; Indels 0; Gaps 0;
QY 3 PNTLCRMSMMLSCIMLMTSWVEGEESOKKLPSSRTICPOGSVAAGSYCYSLIIPOTWSN 62
DB 4 PMAIPSVSMMLSCIMLISQVGEERPELPESARIRCPKSKAYGSHCYALFLSPKSWTD 63
QY 63 AELSCOMHPSGHLAFLSTGEITFYVSSLVKNLSLAYOYIWIIGLHDPHSHGTLPNSSGMKMS 122
DB 64 ADLAQCKRPSGSLVSLGAGSGSVSSLYKSIKNSIYWIIGLHDPHSHGTLPNSSGMKMS 123
QY 123 SSVNLFTYNNERNRNSIAADRGYCAVLSOKSGFQKWRDPNCENELPYICK 171
DB 124 SSDVNNYFAWERNPSTISSPGHCASLSRSTAFELMKDYNCNVRPLPYCK 172
RESULT 12
US-08-422-166-7
Sequence 7, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: pancreas
US-08-422-166-7
Query Match 59.1%; Score 566; DB 2; Length 174;
Best Local Similarity 57.4%; Pred. No. 6.3e-55;
Matches 97; Conservative 34; Mismatches 38; Indels 0; Gaps 0;
QY 3 PNTLCRMSMMLSCIMLMTSWVEGEESOKKLPSSRTICPOGSVAAGSYCYSLIIPOTWSN 62
DB 4 PMAIPSVSMMLSCIMLISQVGEERPELPESARIRCPKSKAYGSHCYALFLSPKSWTD 63
QY 63 AELSCOMHPSGHLAFLSTGEITFYVSSLVKNLSLAYOYIWIIGLHDPHSHGTLPNSSGMKMS 122
DB 64 ADLAQCKRPSGSLVSLGAGSGSVSSLYKSIKNSIYWIIGLHDPHSHGTLPNSSGMKMS 123
QY 123 SSVNLFTYNNERNRNSIAADRGYCAVLSOKSGFQKWRDPNCENELPYICK 171
DB 124 SSDVNNYFAWERNPSTISSPGHCASLSRSTAFELMKDYNCNVRPLPYCK 172
RESULT 13
US-08-822-261-1
Sequence 1, Application US/08822261
Patent No. 5935813
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ISLNOT01
CLONE: 2072483
US-08-822-261-1

Query Match
Best Local Similarity 58.1%; Score 557; DB 2; Length 175;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

Db 3 PNTLCRSMWMLSCIMELFWEGEESOKLPSSRTICOGSVAYGSCYSLILIPQWMSN 62
4 PMALPSYMWLSCILLCVOGEETQKLPSPRISCRGSKAISPCTALFLSPKSMMD 63

Qy 63 AELSCMHPSGHFLAFLSTGETTFVSSLVKNSLTAIYITWIGLHDPHSHGLPNSSGKMS 122
64 ADLACOKRPBGKLYSLAEGSEFVSSLSVRSISNSYIWTIGLHDPHSHGLPNSSGKMS 123

Qy 123 SSNVLFFYWNERNPSIAADRCYAVLSQKSGFQKWRDNCENELPYICRKR 173
124 STVWMTFAWEKRPSTILNPGHGSLSRSTGLKMKDYNCKALPYVCKFK 174

Db 124 STVWMTFAWEKRPSTILNPGHGSLSRSTGLKMKDYNCKALPYVCKFK 174

RESULT 14
US-07-778-156-2
Sequence 2, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPRT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-778-156-2

Query Match
Best Local Similarity 58.1%; Score 557; DB 1; Length 184;
Matches 95; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

Qy 9 MSWMLSCIMELFWEGEESOKLPSSRTICOGSVAYGSCYSLILIPQWMSN 68
10 MSWMLSCIMELFWEGEESOKLPSSRTICOGSVAYGSCYSLILIPQWMSN 69

Db 69 MHSGLAFLSTGETTFVSSLVKNSLTAIYITWIGLHDPHSHGLPNSSGKMS 128
70 KRBEGLVSVLNAVASLAKVKNSTNSYIWTIGLHDPHSHGLPNSSGKMS 129

Qy 129 FYWNERNPSIAADRCYAVLSQKSGFQKWRDNCENELPYICRKR 166
130 YVWERNPSTALDRGFCGLSRSSGFLRMWRTTCEVEV 167

Db 130 YVWERNPSTALDRGFCGLSRSSGFLRMWRTTCEVEV 167

RESULT 15
US-08-422-166-2
Sequence 2, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-Apr-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:46:30 ; Search time 18 seconds
(Without alignments)
730.934 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 958

Sequence: 1 MIPMTICRSMMLSCIMFL.....QKWRDFCENELPYICKFY 174

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Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep: *
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep: *
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	59.7	183	10	US-09-925-301-1013 Sequence 1013, App
2	557	58.1	175	9	US-09-978-285A-452 Sequence 452, App
3	557	58.1	175	9	US-09-978-697-452 Sequence 452, App
4	557	58.1	175	9	US-09-978-192A-452 Sequence 452, App
5	557	58.1	175	9	US-09-999-832A-452 Sequence 452, App
6	557	58.1	175	9	US-09-978-189-452 Sequence 452, App
7	557	58.1	175	9	US-10-174-590-424 Sequence 424, App
8	557	58.1	175	9	US-10-176-758-424 Sequence 424, App
9	557	58.1	175	9	US-10-175-737-424 Sequence 424, App
10	557	58.1	175	9	US-10-173-706-424 Sequence 424, App
11	557	58.1	175	9	US-10-173-728-424 Sequence 424, App
12	557	58.1	175	9	US-10-175-752-424 Sequence 424, App
13	557	58.1	175	9	US-10-176-482-424 Sequence 424, App
14	557	58.1	175	9	US-10-176-757-424 Sequence 424, App
15	557	58.1	175	9	US-10-176-913-424 Sequence 424, App
16	557	58.1	175	9	US-10-180-552-424 Sequence 424, App
17	557	58.1	175	9	US-10-180-557-424 Sequence 424, App
18	557	58.1	175	9	US-10-173-700-424 Sequence 424, App
19	557	58.1	175	9	US-10-174-572-424 Sequence 424, App

20	557	58.1	175	9	US-10-174-579-424 Sequence 424, App
21	557	58.1	175	9	US-10-174-582-424 Sequence 424, App
22	557	58.1	175	9	US-10-174-588-424 Sequence 424, App
23	557	58.1	175	9	US-10-175-739-424 Sequence 424, App
24	557	58.1	175	9	US-10-175-740-424 Sequence 424, App
25	557	58.1	175	9	US-10-175-743-424 Sequence 424, App
26	557	58.1	175	9	US-10-176-488-424 Sequence 424, App
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29	557	58.1	175	9	US-10-176-747-424 Sequence 424, App
30	557	58.1	175	9	US-10-176-985-424 Sequence 424, App
31	557	58.1	175	9	US-10-176-987-424 Sequence 424, App
32	557	58.1	175	9	US-10-176-991-424 Sequence 424, App
33	557	58.1	175	9	US-10-176-992-424 Sequence 424, App
34	557	58.1	175	9	US-10-176-993-424 Sequence 424, App
35	557	58.1	175	9	US-10-184-658-424 Sequence 424, App
36	557	58.1	175	9	US-10-173-695-424 Sequence 424, App
37	557	58.1	175	9	US-10-173-697-424 Sequence 424, App
38	557	58.1	175	9	US-10-173-705-424 Sequence 424, App
39	557	58.1	175	9	US-10-174-576-424 Sequence 424, App
40	557	58.1	175	9	US-10-174-585-424 Sequence 424, App
41	557	58.1	175	9	US-10-174-586-424 Sequence 424, App
42	557	58.1	175	9	US-10-175-747-424 Sequence 424, App
43	557	58.1	175	9	US-10-176-481-424 Sequence 424, App
44	557	58.1	175	9	US-10-176-485-424 Sequence 424, App
45	557	58.1	175	9	US-10-176-487-424 Sequence 424, App

ALIGNMENTS

RESULT 1

US-09-925-301-1013

; Sequence 1013, Application US/09925301

; Patent No. US20020052308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925,301

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05882

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; NUMBER OF SEQ ID NOS: 1694

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1013

; LENGTH: 183

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-925-301-1013

Query Match

Best Local Similarity

Matches 98; Conservative

Mismatches 34; Indels 0; Gaps 0;

3 PWTICRSMMLSCIMFLSWEGEGESOKLPSRINTCPQGSVAGSYCYSLILIPQWSEN 62

12 PVALPSVSMMLSCIMFLSQVQGEPEQRELPSARIRPKSKAYGCHYALFLSPRSTWD 71

63 AELSCOMFHSKHLAFITSTGEITFVSVSVNSLTAAYITWIGLHDPGSHETLPGSKWKS 122

72 ADLACQKRPSSGNLVSLSGALGCSFVSLSVNSIGNSYTWIGLHDPGSHETLPGSKWKS 131

QY 123 SGNVLTFFYNWRNPSIADRGCAVLSQSKSGFQKWRDFCENELPYICKFY 172

DB 132 SSDVANYFWARNPSTLSSPGHCASLRSRTAFLEMKDYNCNVALPYCKF 181

RESULT 2

US-09-978-295A-452

; Sequence 452, Application US/09978295A

Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Iyar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/916585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29

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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
QY 3 PWTICRMNMLSCIMFTSWVEGESOKKLPSSRTCPQGSVAVYGSYSLIPQWTSN 62
DB 4 PMALPVSVMWLLSCILLCQVGEETQKLEPSPRISCKGSKAVGSPCYALFSPKXMD 63
QY 63 AELSCOMHSHGLAFLTSGELTYVSSLYXNSLTAYQITWIGLHDPISGCTIPNSGKMS 122
DB 64 ADLACORRPSGKLVSLSABSGSVSLVRSLSNSISTYIMIGLHDPYQGSSEDDGEMWS 123
QY 123 SSNVLFYFWERNPISLAADRGYCAVLISQKSGFQKWWDENCENELPYICKFK 173
DB 124 STDVMYFAMEKNPSTILNPHGCSLSRSTGFLFKKDYNCDAKLPYCKFK 174

RESULT 3
US-09-978-697-452

;; Sequence 452, Application US/09978697
;; Patent No. US20020169284A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Flivarov, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaud, J. Christopher
;; APPLICANT: Gunney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kiljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC27
;; CURRENT APPLICATION NUMBER: US/09/978,697
;; PRIOR FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
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;; PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 58.1%, Score 557, DB 9, Length 175;
Best Local Similarity 55.6%, Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PPTLCMSWMLISCLMFSLWYBESQKLPSSRTTPQGSVAVAGSCYLLILPOTWSN 62
DB 4 PMLPSVSWMLISCLILCOVOGEBTQKLPSPRISCPKSGKAYGSPVALPFSKSWMD 63
QY 63 AELSCQMHPSGHIAPLSTGETFEVSSLYKNSLTAYOYIWTGLHDPHGTLPNQSGKWS 122
DB 64 ADLACQKRPQSGKLYVLSGABQSPFVSLVRSISNSYSYIWTGLHDPQGSBPQDQWMS 123
QY 123 SSVVLFTYMWENRPSIADRGYCAVLSSQSGFQWWRPQNCENELPYCKRK 173
DB 124 SDVYNYFAWEKNPSTILNPGHCSLSRSTGFLMKDYNCDAKLYVCKRK 174
RESULT 4

US-09-978-192A-452
; Sequence 452, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 58.1%; Score 557; DB 9; Length 175;
Best local Similarity 55.6%; Pred. No. 2, Re-48;

Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

OY 3 PMTLCRSMWMLSCMLFSLWGEESOKLPPSSRTTCOGSVAVGSCYYSLLIPQWNS 62
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OY 63 AESLCMHFSGHLAPLSTGEITFVSSLYKNSLFTYQYITWIGLHDPSPSHGTLPPNGSGKWS 122
DB 64 ADLACQKRPBGKLYVLSGABEGSFVSLVRSISNSTYITWIGLHDPSPSGEDGSGWS 123
OY 123 SSNVLFYFWMERNPSTADRGTCVAVISQKSGFKRNDCEENELPYICKFK 173
DB 124 STDVMMYFAWEKNPSTILNPGHGSLSRSTGFLKWKDYNCDAKLPYCKFK 174

RESULT 5
US-09-999-832A-452
Sequence 452, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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11	PRIOR FILING DATE: 1998-04-29
12	PRIOR APPLICATION NUMBER: 60/083500
13	PRIOR FILING DATE: 1998-04-29
14	PRIOR APPLICATION NUMBER: 60/083742
15	PRIOR FILING DATE: 1998-04-30
16	PRIOR APPLICATION NUMBER: 60/084366
17	PRIOR FILING DATE: 1998-05-05
18	PRIOR APPLICATION NUMBER: 60/084414
19	PRIOR FILING DATE: 1998-05-06
20	PRIOR APPLICATION NUMBER: 60/084441
21	PRIOR FILING DATE: 1998-05-06
22	PRIOR APPLICATION NUMBER: 60/084637
23	PRIOR FILING DATE: 1998-05-07
24	PRIOR APPLICATION NUMBER: 60/084639
25	PRIOR FILING DATE: 1998-05-07
26	PRIOR APPLICATION NUMBER: 60/084640
27	PRIOR FILING DATE: 1998-05-07
28	PRIOR APPLICATION NUMBER: 60/084598
29	PRIOR FILING DATE: 1998-05-07
30	PRIOR APPLICATION NUMBER: 60/084600
31	PRIOR FILING DATE: 1998-05-07
32	PRIOR APPLICATION NUMBER: 60/084627
33	PRIOR FILING DATE: 1998-05-07
34	PRIOR APPLICATION NUMBER: 60/084643
35	PRIOR FILING DATE: 1998-05-07
36	PRIOR APPLICATION NUMBER: 60/085339
37	PRIOR FILING DATE: 1998-05-13
38	PRIOR APPLICATION NUMBER: 60/085338
39	PRIOR FILING DATE: 1998-05-13
40	PRIOR APPLICATION NUMBER: 60/085323
41	PRIOR FILING DATE: 1998-05-13
42	PRIOR APPLICATION NUMBER: 60/085382
43	PRIOR FILING DATE: 1998-05-15
44	PRIOR APPLICATION NUMBER: 60/085700
45	PRIOR FILING DATE: 1998-05-15
46	PRIOR APPLICATION NUMBER: 60/085689
47	PRIOR FILING DATE: 1998-05-15
48	PRIOR APPLICATION NUMBER: 60/085779
49	PRIOR FILING DATE: 1998-05-15
50	PRIOR APPLICATION NUMBER: 60/085580
51	PRIOR FILING DATE: 1998-05-15
52	PRIOR APPLICATION NUMBER: 60/085573
53	PRIOR FILING DATE: 1998-05-15
54	PRIOR APPLICATION NUMBER: 60/085704
55	PRIOR FILING DATE: 1998-05-15
56	PRIOR APPLICATION NUMBER: 60/085697

Query Match	58.1%;	Score 557;	DB 9;	Length 175;
Best Local Similarity	55.6%;	Pred. No. 2.8e-48;		
Matches	95;	Conservative 37;	Mismatches 39;	Indels 0;
			Gaps	0;

[illegible]

RESULT 6
US-09-978-189-452
Sequence 452, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664

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PRIOR APPLICATION NUMBER: 60/079663
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
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PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29

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/ PRIOR APPLICATION NUMBER: 60/083496
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083499
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
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/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match      58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
```

```
QY 3 PNTLCMSMMLSCIMFISWVEGESQKLPSSRTCPQSGVAAGYCYSLILPQWMSN 62
DB 4 PALPSVSMMLSCILICOVGEETQKELPSRISCKSGKAYGSCYALFLSPKSMWD 63
QY 63 AELSCOMHPSGHLAFLSTGETTFVSSLVKNLSLAYQYIWIGLDPSHGLTPNBSGKWS 122
DB 64 ADIACOKRPSGGLVSLGABSGFVSSLYRSISNSYIWIWGLDPTQSGSPDDGKWS 123
QY 123 SSNVLTFFWERNPSTIAADRGYCAVLISQSGFQKWRDNCENELPYICKER 173
DB 124 STDVMTFFWERNPSTILNPGHGSLSRSTGTLKWKDYNCDAKLPYICKER 174
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```
RESULT 7
US-10-174-590-424
/ Sequence 424, Application US/10174590
/ Publication No. US2003008352A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Goddard, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Zhang, Zemin I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C42
/ CURRENT APPLICATION NUMBER: US/10/174,590
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 424
/ LENGTH: 175
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-174-590-424
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```
Query Match      58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PNTLCMSMMLSCIMFISWVEGESQKLPSSRTCPQSGVAAGYCYSLILPQWMSN 62
DB 4 PALPSVSMMLSCILICOVGEETQKELPSRISCKSGKAYGSCYALFLSPKSMWD 63
QY 63 AELSCOMHPSGHLAFLSTGETTFVSSLVKNLSLAYQYIWIWGLDPSHGLTPNBSGKWS 122
DB 64 ADIACOKRPSGGLVSLGABSGFVSSLYRSISNSYIWIWGLDPTQSGSPDDGKWS 123
QY 123 SSNVLTFFWERNPSTIAADRGYCAVLISQSGFQKWRDNCENELPYICKER 173
DB 124 STDVMTFFWERNPSTILNPGHGSLSRSTGTLKWKDYNCDAKLPYICKER 174
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RESULT 8
US-10-176-758-424
/ Sequence 424, Application US/10176758
/ Publication No. US2003008353A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Goddard, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C104
/ CURRENT APPLICATION NUMBER: US/10/176,758
/ PRIOR FILING DATE: 2002-06-21
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 424
/ LENGTH: 175
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-424

```

Query Match	58.1%;	Score 557;	DB 9;	Length 175;
Best Local Similarity	55.6%;	Pred. No. 2.8e-48;		
Matches 95;	Conservative 37;	Mismatches 39;	Indels 0;	Gaps 0;

```

QY - 3 PMLICRSMWMLSLTMLNWEGEREOKRPPSRICPOSSVAVGYSCYLLIPOTSM 62
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 4 PMLAPSWMLSLCILCOVQGEETKEPLSPRISCPKSKAYGSCYALFLSPKSM 63
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 63 AELSCOMHPSCHLAFLLSTGEHTFVSSLVKNSLTAOYIWLGLHDSHGTLPMGSCMKMS 122
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 64 ADLACORRPSCKLTVSLTSGAEFSSVLSYLSINSYSYIWLGLHDPQSSGPDGDGEMWS 123
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 123 SSNVLTFEYMERNPISADRGYCAVLQKSGFOKMRDNCENELPYTCRER 173
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 124 STDVAMNFAEMKRNSTLLNPQHCSTLRSRQGLFMKRYINDAKLPHYCRER 174
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 9
US-10-175-737-424

Query Match	58.1%;	Score 557;	DB 9;	Length 175;
Best Local Similarity	55.6%;	Pred. No. 2.8e-48;		
Matches	95;	Conservative 37;	Mismatches 39;	Indels 0;
				Gaps 0;

[illegible]

RESULT 10
US-10-173-706-424
; Sequence 424, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

? APPLICANT: Chen, Jian
? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zhenlu
? TITLE OF INVENTION: ACIDS ENCODING THE SAME
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3430R1C7
? CURRENT APPLICATION NUMBER: US/10/173,706
? CURRENT FILING DATE: 2002-06-17
? Prior Application removed - See file Wrapper or Palm
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 424
? LENGTH: 175
? TYPE: PRT
? ORGANISM: Homo Sapien
? US-10-173-706-424

```

Query Match	58.1%;	Score 557;	DB 9;	Length 175;
Best Local Similarity	55.6%;	Pred. No. 2.8e-48;		
Matches 95;	Conservative 37;	Mismatches 39;	Indels 0;	Gaps 0;

[illegible]

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1      RESULT 11
2      ; Sequence 424, Application US/10175738
3      ; Publication No. US20030022294A1
4      ; GENERAL INFORMATION:
5      ; APPLICANT: Baker, Kevin P.
6      ; APPLICANT: Chen, Jian
7      ; APPLICANT: Desnoyers, Luc
8      ; APPLICANT: Goddard, Audrey
9      ; APPLICANT: Godowski, Paul J.
10     ; APPLICANT: Guirney, Austin L.
11     ; APPLICANT: Pan, James
12     ; APPLICANT: Smith, Victoria
13     ; APPLICANT: Watanabe, Colin K.
14     ; APPLICANT: Wood, William I.
15     ; APPLICANT: Zhang, Zemin
16     ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
17     ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
18     ; FILE REFERENCE: P3430R1C45
19     ; CURRENT APPLICATION NUMBER: US/10/175,738
20     ; CURRENT FILING DATE: 2002-06-19
21     ; Prior application removed - See File Wrapper or Palm
22     ; NUMBER OF SEQ ID NOS: 612
23     ; SEQ ID NO 424
24     ; LENGTH: 175
25     ; TYPE: PRT
26     ; ORGANISM: Homo Sapien
27     ; US-10-175-738-424

```

Query Match	58.1%;	Score 557;	DB 9;	Length 175;
Best Local Similarity	55.6%;	Pred. No. 2.8e-48;		
Matches 95: Conservative	37;	Mismatches 39;	Indels 0;	Gaps 0;

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:46:51 ; Search time 36 seconds

(without alignments)
644.045 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MIPMTLCRMSWMLSCIMFL.....QKWRDPCENELPYICKRY 174

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 10

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	174	AA98525	Hamster islet neog
2	174	100.0	175	AAW64790	INGAP protein frag
3	25	14.4	26	AAW64789	INGAP signal pepti
4	25	14.4	26	AAW55049	INGAP coding sequ
5	21	12.1	21	ABB79542	Hamster islet neog
6	15	8.6	15	ABB79543	Hamster islet neog
7	14	8.0	14	ABB79544	Hamster islet neog
8	14	8.0	14	ABB79545	Hamster islet neog
9	10	5.7	175	AAW34097	Mouse PAP. Mus mu
10	10	5.7	175	AAW95089	Reg-2 protein. Ra

11 10 5.7 175 21 AAR18614
12 10 5.7 184 12 AAR14797

Amino acid sequenc
Rat pancreatitis a

ALIGNMENTS

RESULT 1

AA98525 standard; Protein; 174 AA.

AA98525:

18-APR-1997 (first entry)

Hamster islet neogenesis associated protein.

Hamster; islet neogenesis associated protein; INGAP; pancreas; endocrine; proliferation; pancreatic tissue; cellophane; duct epithelium; homology; differential display method; open reading frame; liver; adenocarcinoma; pancreatitis associated protein; lithostatine; pancreatic stone protein; beta-cell; regeneration; insulin; diabetes; mammal.

Cricetulus sp.

MO9626215-A1.

29-AUG-1996.

12-FEB-1996; 96WO-0501528.

07-NOV-1995; 95US-0006271.

22-FEB-1995; 95US-0401530.

(EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L;

Vinik AI;

WPI; 1996-402318/40.

N-PSDB; AAT36612.

Mammalian islet neogenesis associated protein - isolated by stimulating mammalian pancreas by wrapping in cellophane, for treatment of diabetes, etc

Claim 2; Page 26; 50pp; English.

This is the amino acid sequence of the hamster islet neogenesis associated protein (INGAP). The gene is isolated from pancreatic cells which are induced to proliferate upon wrapping pancreatic tissue in cellophane. Wrapping of the pancreas stimulate proliferation of new endocrine cells which appear from duct epithelium. The INGAP gene was isolated from a cDNA library constructed from mRNA purified from cellophane wrapped hamster pancreas using a differential display method to compare genes expressed in cellophane-wrapped and control pancreas. The gene contains an open reading frame which encodes a protein of 175 amino acids. The protein has structural homology to the pancreatitis associated protein (PAP)/HIP family of genes which is associated with pancreatic or liver adenocarcinoma, and to the Reg/PSPI/lithostatine (PSP - pancreatic stone protein) family of gene which has been shown to stimulate pancreatic beta-cell growth and may be involved in pancreatic islet regeneration. The protein can be used to stimulate islet cell proliferation in (non-)insulin dependent diabetic mammals.

Sequence 174 AA;

Query Match 100.0%; Score 174; DB 17; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-174;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MIPMTLCRMSWMLSCIMFLSWBESQKLPSSRTTCQGSVAAGSTCYSLIPQTM 60
|||||

Db 1 MLPNTLCRSMWMLISCLMFLSMWVEGESQKLPSSRITCPGGSVAVGSYCYSLILIPQTW 60
 OY 61 SNAEISCOMHESGHIAFLISTGTEITFVSVLYKNSLITAVOYIWIIGLHDSHGTLPNGSGWK 120
 Db 61 SNAEISCOMHESGHIAFLISTGTEITFVSVLYKNSLITAVOYIWIIGLHDSHGTLPNGSGWK 120
 OY 121 WSSSNVLTFFYNMERNPISIAADRGYCAVLISQKSGFQKMDFCENELPYICKFKY 174
 Db 121 WSSSNVLTFFYNMERNPISIAADRGYCAVLISQKSGFQKMDFCENELPYICKFKY 174

RESULT 2

AAW64790
 ID AAW64790 standard; Protein: 175 AA.

AAW64790;

18-NOV-1998 (first entry)

DE INGAP protein fragment.

KW INGAP; islet neogenesis-associated protein; treatment; diabetes;
 host cell.

OS Unknown.

PN US5804421-A.

PD 08-SEP-1998.

PF 12-AUG-1997; 97US-0909725.

PR 12-AUG-1997; 97US-0909725.

PR 30-OCT-1996; 96US-0741096.

PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

PI Barlow SM, Pittenger GL, Rafaeloff-Phail R, Vink AI;

DR WPI; 1998-505656/43.

PT Expression of islet neogenesis-associated protein - from recombinant

PT construct lacking signal peptide, useful in the treatment of

PT diabetes

PS Claim 1; Column 19-20; 14pp; English.

XX This sequence represents INGAP, an islet neogenesis-associated protein.

CC This sequence is used in the construction of a recombinant construct

CC having a coding sequence lacking a signal sequence and which is operably

CC linked to transcription and translation initiation sites. This construct

CC in a host cell is useful for producing recombinant mature INGAP, which

CC is useful in the treatment of diabetes. High levels of INGAP expression

CC can be achieved in bacterial and eukaryotic cells by removing the signal

CC peptide as it is possibly toxic to cells.

XX Sequence 175 AA:

Query Match 100.0%; Score 174; DB 19; Length 175;

Best Local Similarity 100.0%; Pred. No. 1.5e-174; Mismatches 0; Indels 0; Gaps 0;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPNTLCRSMWMLISCLMFLSMWVEGESQKLPSSRITCPGGSVAVGSYCYSLILIPQTW 60

Db 2 MLPNTLCRSMWMLISCLMFLSMWVEGESQKLPSSRITCPGGSVAVGSYCYSLILIPQTW 61

OY 61 SNAEISCOMHESGHIAFLISTGTEITFVSVLYKNSLITAVOYIWIIGLHDSHGTLPNGSGWK 120

Db 62 SNAEISCOMHESGHIAFLISTGTEITFVSVLYKNSLITAVOYIWIIGLHDSHGTLPNGSGWK 121

OY 121 WSSSNVLTFFYNMERNPISIAADRGYCAVLISQKSGFQKMDFCENELPYICKFKY 174

Db 122 WSSSNVLTFFYNMERNPISIAADRGYCAVLISQKSGFQKMDFCENELPYICKFKY 175

RESULT 3
 AAW64789
 ID AAW64789 standard; Protein: 26 AA.

AAW64789;

18-NOV-1998 (first entry)

DE INGAP signal peptide.

KW INGAP; islet neogenesis-associated protein; treatment; diabetes;

KW host cell.

OS Unknown.

PN US5804421-A.

PD 08-SEP-1998.

PF 12-AUG-1997; 97US-0909725.

PR 12-AUG-1997; 97US-0909725.

PR 30-OCT-1996; 96US-0741096.

PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

PI Barlow SM, Pittenger GL, Rafaeloff-Phail R, Vink AI;

DR WPI; 1998-505656/43.

PT Expression of islet neogenesis-associated protein - from recombinant

PT construct lacking signal peptide, useful in the treatment of

PT diabetes

PS Example 1; Column 17-20; 14pp; English.

XX This cDNA sequence is the signal peptide of INGAP, an islet

CC neogenesis-associated protein. This sequence is removed during the

CC construction of a recombinant construct which has a coding

CC sequence lacking a signal sequence and which is operably linked to

CC transcription and translation initiation sites. This construct in a host

CC cell is useful for producing recombinant mature INGAP, which is useful in

CC the treatment of diabetes. High levels of INGAP expression can be

CC achieved in bacterial and eukaryotic cells by removing the signal peptide

CC as it is possibly toxic to cells.

XX Sequence 26 AA:

Query Match 14.4%; Score 25; DB 19; Length 26;

Best Local Similarity 100.0%; Pred. No. 8.7e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPNTLCRSMWMLISCLMFLSMWVEGES 25

Db 2 MLPNTLCRSMWMLISCLMFLSMWVEGES 26

RESULT 4
 AAW55049
 ID AAW55049 standard; Peptide: 26 AA.

AAW55049;

25-SEP-1998 (first entry)

DE INGAP coding sequence signal peptide.

KW INGAP; pancreas; Iliotropin; islets of Langerhans; diabetes mellitus.

OS Mammalia.

XX PN WO9818913-A1.
 XX PD 07-MAY-1998.
 XX PF 30-OCT-1997; 97WO-US19415.
 XX PR 30-OCT-1996; 96US-0741096.
 XX PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
 XX PI Barlow SM, Pittenger GI, Rafaeloff R, Vinik AI;
 XX DR WPI; 1998-272209/24.
 XX DR N-PSDB; AAV30281.
 XX PS Claim 2; Page 5; 22pp; English.
 CC The INAP signal peptide and the 5' UTR were excluded from a recombinant
 CC construct for expressing INAP activity containing a nucleotide sequence
 CC encoding amino acids 27-175 of INAP operably linked to a transcription
 CC initiation site and a translational initiation site. The construct can
 CC be used to produce biologically active INAP, by culturing the
 CC transformed host cells. INAP is found within a pancreatic extract
 CC called islet tropin and is known to be responsible for stimulating cell
 CC regeneration of the pancreatic islets of Langerhans. The INAP produced
 CC is useful in treatments to regenerate the islets of Langerhans to prevent
 CC or ameliorate the symptoms of diabetes mellitus. Previous methods have
 CC produced only low yields of INAP, possibly because the INAP signal
 CC sequence is toxic to bacteria.
 XX SQ Sequence 26 AA;
 Query Match 14.4%; Score 25; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8,7e-19;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPMTCRMSMMLSCIMFLSWVEG 25
 DB 2 MLPMTCRMSMMLSCIMFLSWVEG 26
 RESULT 5
 ABB79542
 ID ABB79542 standard; Peptide; 21 AA.
 XX AC ABB79542;
 XX DT 01-OCT-2002 (first entry)
 XX DE Hamster islet neogenesis associated protein (INGAP) immunogen.
 XX KW Islet neogenesis associated protein; INGAP; immunogen; hamster;
 XX KM pancreas; diabetes; immunoassay.
 XX OS Cricetus sp.
 XX PN WO200256028-A2.
 XX PD 18-JUL-2002.
 XX PF 08-JAN-2002; 2002WO-US00071.
 XX PR 09-JAN-2001; 2001US-260210P.
 XX PR 07-JAN-2002; 2002US-0036418.
 XX PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
 XX PI Vinik AI, Taylor-Fishwick D;

XX DR WPI; 2002-557841/59.
 XX PT Assaying islet neogenesis associated protein (INGAP) for treating
 XX PT diabetes types I and II, comprises determining the amount of labeled
 XX PT INAP molecule bound to antibodies or to a solid support comprising the
 XX PT bound antibodies
 XX PS Claim 1; Page 12; 29pp; English.
 XX The present sequence is a peptide immunogen corresponding to amino
 XX acid residues 20-40 of full-length hamster islet neogenesis
 XX associated protein (INGAP). The invention provides methods for
 XX assaying INAP in a test sample. In a competitive binding assay,
 XX antibodies which specifically bind to the INAP immunogen are
 XX contacted with a test sample which may contain INAP protein, and a
 XX labeled INAP molecule, e.g. a fusion protein comprising INAP
 XX protein and a marker protein. The amount of labeled INAP
 XX molecule bound to the antibodies is determined. This amount is
 XX inversely related to INAP protein in the test sample. Antibodies
 XX raised against different INAP immunogens (see ABB79543-45) and
 XX their subfragments may also be used. They may be monoclonal or
 XX polyclonal, may be bound to a solid support, and do not specifically
 XX bind to other portions of the INAP protein or to other human
 XX proteins. The method can be used to determine the amount of INAP
 XX e.g. in culture media or biological tissues and fluids. The
 XX ability to assay INAP will facilitate the full exploitation of
 XX this protein for fighting human disease, such as diabetes types I
 XX and II.
 XX SQ Sequence 21 AA;
 Query Match 12.1%; Score 21; DB 23; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 FLSWVEGESQKRLPSSRITC 39
 DB 1 FLSWVEGESQKRLPSSRITC 21
 RESULT 6
 ABB79543
 ID ABB79543 standard; Peptide; 15 AA.
 XX AC ABB79543;
 XX DT 01-OCT-2002 (first entry)
 XX DE Hamster islet neogenesis associated protein (INGAP) immunogen.
 XX KW Islet neogenesis associated protein; INGAP; immunogen; hamster;
 XX KM pancreas; diabetes; immunoassay.
 XX OS Cricetus sp.
 XX PN WO200256028-A2.
 XX PD 18-JUL-2002.
 XX PF 08-JAN-2002; 2002WO-US00071.
 XX PR 09-JAN-2001; 2001US-260210P.
 XX PR 07-JAN-2002; 2002US-0036418.
 XX PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
 XX PI Vinik AI, Taylor-Fishwick D;
 XX DR WPI; 2002-557841/59.
 XX PT Assaying islet neogenesis associated protein (INGAP) for treating
 XX PT diabetes types I and II, comprises determining the amount of labeled

PT INCAP molecule bound to antibodies or to a solid support comprising the
PT bound antibodies
XX
XX
PS. Claim 24; Page 14; 29pp; English.
XX
CC The present sequence is a peptide immunogen corresponding to amino
CC acid residues 104-118 of full-length hamster islet neogenesis
CC associated protein (INGAP). The invention provides methods for
CC assaying INCAP in a test sample. In a competitive binding assay,
CC antibodies which specifically bind to the INCAP immunogen are
CC contacted with a test sample which may contain INCAP protein, and a
CC labeled INCAP molecule, e.g. a fusion protein comprising INCAP
CC protein and a marker protein. The amount of labeled INCAP
CC molecule bound to the antibodies is determined. This amount is
CC inversely related to INCAP protein in the test sample. Antibodies
CC raised against different INCAP immunogens (see ABB79542-45) and
CC their subfragments may also be used. They may be monoclonal or
CC polyclonal, may be bound to a solid support, and do not specifically
CC bind to other portions of the INCAP protein or to other human
CC proteins. The method can be used to determine the amount of INCAP
CC e.g. in culture media or biological tissues and fluids. The
CC ability to assay INCAP will facilitate the full exploitation of
CC this protein for fighting human disease, such as diabetes types I
CC and II.
XX
SQ Sequence 15 AA;
Query Match 8.6%; Score 15; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 IGLHDPHSGTLPNGS 117
Db 1 IGLHDPHSGTLPNGS 15
|||||
RESULT 7
ABB79544
ID ABB79544 standard; Peptide; 14 AA.
XX
AC ABB79544;
XX
DT 01-OCT-2002 (first entry)
XX
DE Hamster islet neogenesis associated protein (INGAP) immunogen.
XX
KW Islet neogenesis associated protein; INCAP; immunogen; hamster;
KW pancreas; diabetes; immunoassay.
XX
OS Cricetus sp.
XX
PN WO200256028-A2.
XX
PD 18-JUL-2002.
XX
PE 08-JAN-2002; 2002WO-US00071.
XX
PR 09-JAN-2001; 2001US-260210P.
PR 07-JAN-2002; 2002US-0036418.
XX
PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
XX
PI Vlnik AI, Taylor-Fishwick D;
XX
DR WPI; 2002-557841/59.
XX
PT Assaying islet neogenesis associated protein (INGAP) for treating
PT diabetes types I and II, comprises determining the amount of labeled
PT INCAP molecule bound to antibodies or to a solid support comprising the
PT bound antibodies
XX
PS Claim 24; Page 14; 29pp; English.

CC The present sequence is a peptide immunogen corresponding to amino
CC acid residues 139-152 of full-length hamster islet neogenesis
CC associated protein (INGAP). The invention provides methods for
CC assaying INCAP in a test sample. In a competitive binding assay,
CC antibodies which specifically bind to the INCAP immunogen are
CC contacted with a test sample which may contain INCAP protein, and a
CC labeled INCAP molecule, e.g. a fusion protein comprising INCAP
CC protein and a marker protein. The amount of labeled INCAP
CC molecule bound to the antibodies is determined. This amount is
CC inversely related to INCAP protein in the test sample. Antibodies
CC raised against different INCAP immunogens (see ABB79542-45) and
CC their subfragments may also be used. They may be monoclonal or
CC polyclonal, may be bound to a solid support, and do not specifically
CC bind to other portions of the INCAP protein or to other human
CC proteins. The method can be used to determine the amount of INCAP
CC e.g. in culture media or biological tissues and fluids. The
CC ability to assay INCAP will facilitate the full exploitation of
CC this protein for fighting human disease, such as diabetes types I
CC and II.
XX
SQ Sequence 14 AA;
Query Match 8.0%; Score 14; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 IADRGYCAVLSQK 151
Db 1 IADRGYCAVLSQK 14
|||||
RESULT 8
ABB79545
ID ABB79545 standard; Peptide; 14 AA.
XX
AC ABB79545;
XX
DT 01-OCT-2002 (first entry)
XX
DE Hamster islet neogenesis associated protein (INGAP) immunogen.
XX
KW Islet neogenesis associated protein; INCAP; immunogen; hamster;
KW pancreas; diabetes; immunoassay.
XX
OS Cricetus sp.
XX
PN WO200256028-A2.
XX
PD 18-JUL-2002.
XX
PE 08-JAN-2002; 2002WO-US00071.
XX
PR 09-JAN-2001; 2001US-260210P.
PR 07-JAN-2002; 2002US-0036418.
XX
PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
XX
PI Vlnik AI, Taylor-Fishwick D;
XX
DR WPI; 2002-557841/59.
XX
PT Assaying islet neogenesis associated protein (INGAP) for treating
PT diabetes types I and II, comprises determining the amount of labeled
PT INCAP molecule bound to antibodies or to a solid support comprising the
PT bound antibodies
XX
PS Claim 24; Page 14; 29pp; English.
XX
CC The present sequence is a peptide immunogen corresponding to amino
CC acid residues 151-164 of full-length hamster islet neogenesis
CC associated protein (INGAP). The invention provides methods for
CC assaying INCAP in a test sample. In a competitive binding assay,
CC antibodies which specifically bind to the INCAP immunogen are

CC contacted with a test sample which may contain INGP protein, and a
 CC labelled INGP molecule, e.g. a fusion protein comprising INGP
 CC protein and a marker protein. The amount of labelled INGP
 CC molecule bound to the antibodies is determined. This amount is
 CC inversely related to INGP protein in the test sample. Antibodies
 CC raised against different INGP immunogens (see AB87942-45) and
 CC their subfragments may also be used. They may be monoclonal or
 CC polyclonal, may be bound to a solid support, and do not specifically
 CC bind to other portions of the INGP protein or to other human
 CC proteins. The method can be used to determine the amount of INGP
 CC e.g. in culture media or biological tissues and fluids. The
 CC ability to assay INGP will facilitate the full exploitation of
 CC this protein for fighting human disease, such as diabetes types I
 CC and II.

CC
 XX
 SQ Sequence 14 AA;

Query Match 8.0%; Score 14; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 QKSGFQKWRDNC 163
 DB 1 QKSGFQKWRDNC 14

RESULT 9

AAR54097
 ID AAR54097 standard; Protein; 175 AA.

AC AAR54097;

DT 01-FEB-1995 (first entry)

DE Mouse PAP.

KM Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
 aggregation; antibacterial; primer; PCR.

OS Mus musculus.

PN JP06135998-A.

PD 17-MAY-1994.

PF 22-OCT-1992; 92UP-0284765.

PR 22-OCT-1992; 92UP-0284765.

PA (SHIO) SHIONOGI & CO LTD.

DR WPI; 1994-197103/24.

DR N-PSDB; AAO64171.

PT Human and mouse pancreatitis-associated protein (PAP) - useful
 for prep. of proteaceous antibacterial agent

PS Claim 1-6; Page 5-6; 7pp; Japanese.

CC PAP DNA has a high bacteria-aggregating activity and is useful for
 CC the prep. of PAP which can act as a proteaceous antibacterial
 CC agent. Total RNA was isolated from mouse. It was hybridised with a
 CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
 CC Two primers are given in AAO64173-74.

CC
 XX
 SQ Sequence 175 AA;

Query Match 5.7%; Score 10; DB 15; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSWMLSLCLM 18
 XX

DB 10 MSWMLSLCLM 19

RESULT 10

AAM95089
 ID AAM95089 standard; Protein; 175 AA.

AC AAM95089;

DT 20-MAY-1999 (first entry)

DE Reg-2 protein.

KM Reg-2; Schwann cell mitogen; repair; regenerate; neuronal cell; tissue;
 glial growth factor; neuroglin.

OS Rattus sp.

PN GB2329335-A.

PD 24-MAR-1999.

PF 16-SEP-1998; 98GB-0020193.

PR 17-SEP-1997; 97GB-0019796.

PA (MEDIC) MEDICAL RES COUNCIL.

PI Hunt SP, Livsey FJ;

DR WPI; 1999-156299/14.

DR N-PSDB; AAX26126.

PT Use of a protein (Reg-2) to manufacture a Schwann cell mitogen, -- to
 repair and/or regenerate neuronal cells or tissue, either in vivo,
 or in vitro and then introduced into subject

PS Claim 1; Page 24; 33pp; English.

CC The invention relates to the use of a protein (Reg-2) or its variant,
 CC derivative or homologue to manufacture a Schwann cell mitogen. Reg-2 is
 CC used to repair and/or regenerate neuronal cells or tissue. Neuronal cells
 CC or tissue may be repaired and/or regenerated either in vivo, or in vitro
 CC and then introduced into a subject. Reg-2 unlike known Schwann cell
 CC mitogens e.g. glial growth factors/neuroglins, are upregulated during
 CC regeneration. The present sequence represents the Reg-2 protein.

CC
 XX
 SQ Sequence 175 AA;

Query Match 5.7%; Score 10; DB 20; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSWMLSLCLM 18
 DB 10 MSWMLSLCLM 19

RESULT 11

AAB18614
 ID AAB18614 standard; Protein; 175 AA.

AC AAB18614;

DT 15-JAN-2001 (first entry)

DE Amino acid sequence of a rat Reg-2 polypeptide.

KM Schwann cell mitogen; Reg-2; neuronal cell regeneration; motor neuron;
 neuron-glial interaction.

OS Rattus sp.
 XX

```

PN GB2347931-A.
XX
XX 20-SEP-2000.
XX
XX 02-FEB-2000; 2000GB-0002424.
XX
XX 17-SEP-1997; 97GB-0019796.
XX PR 16-SEP-1998; 98GB-0020193.
XX
XX (MED1-) MEDICAL RES COUNCIL.
XX
XX Livesey FJ, Hunt SP;
XX
XX WPI; 2000-567204/53.
XX DR N-PSDB; AAA75486.
XX
XX New Schwann cell mitogen (known as Reg-2), useful for repair and
XX regeneration of neuronal cells and tissue, is upregulated during
XX neuronal regeneration -
XX
XX Claim 2; Page 24; 32pp; English.
XX
XX The present sequence represents a Schwann cell mitogen, known as Reg-2.
XX Reg-2 can be upregulated during regeneration of neuronal cells and
XX tissue. Reg-2 is an essential component in neuron-glia interaction
XX that underlies development and regeneration of mammalian motor
XX neurons. It is a 16 kDa protein. Reg-2 is used to affect development
XX of neuronal cells and tissue, especially for promoting their repair
XX and regeneration, particularly of motor cells in adult humans.
XX
XX
SQ Sequence 175 AA;
Query Match 5.7%; Score 10; DB 21; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

RESULT 12
AAR14797
ID AAR14797 standard; Protein; 184 AA.
XX
XX AAR14797;
XX
XX 29-JAN-1992 (first entry)
XX
XX Rat pancreatitis associated protein A1.
XX
XX hPAP; pancreas; imaging.
XX
XX Rattus.
XX
XX OS
XX
XX Key Location/Qualifiers
XX FH 1..26
XX FT Peptide 27..184
XX FT Protein /label= mature PAP
XX
XX WO9116428-A.
XX
XX PN
XX
XX 31-OCT-1991.
XX
XX
XX 18-APR-1991; 91WO-FR00323.
XX PF
XX
XX 20-APR-1990; 90FR-0005062.
XX PR
XX
XX (INRM ) INSERM INST NAT SANTE.
XX PA
XX
XX Iovanna JL, Keim V, Dagron JC;
XX PI
XX
XX WPI; 1991-339816/46.
XX DR

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DR N-PSDB; AAQ14621.
XX
XX cDNA fragment of human pancreatitis associated protein -
XX PT produced by genetic engineering, and the corresponding antibody,
XX PT for use in the diagnosis of pancreatitis
XX
XX Claim 16; Page 34; 49pp; French.
XX
XX
XX The cDNA fragment SI encoding the rat PAP was isolated from a rat
XX pancreatic cDNA library using antibodies against rat PAP.
XX
XX
XX Sequence 184 AA;
Query Match 5.7%; Score 10; DB 12; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

```

Search completed: April 16, 2003, 10:49:28
Job time : 37 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:48:26 (Search time 17 seconds)

(Without alignments) 983.964 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 174
1 MIPMTLCRMSMMLSLCLMFL.....OKWRDPCENNELPYICKKRV 174

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 10

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	10	5.7	175	A41719	pancreatic stone p
2	10	5.7	175	S29822	pancreatitis-assoc

ALIGNMENTS

RESULT 1
A41719
N:Alternate names: pancreatic stone 2 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 20-Jun-2000
C/Accession: A37456; A59313; I51899; JCI257; A41719
R/Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
J. Biol. Chem. 268, 14470-14475, 1993
A/Title: Structural organization of the gene encoding the rat pancreatitis-associated pr
on domain-containing genes.
A/Reference number: A37456; MUID:93300847; PMID:8314803
A/Accession: A37456
A/Molecule type: DNA
A/Residues: 1-175 <DUS1>
A/Cross-references: GB:I07127; NID:9349550
A/Note: only intron/exon boundaries are shown; exon I and the beginning of exon II are c
R/Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
submitted to GenBank, August 1993
A/Reference number: A59313

A/Accession: A59313
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 'MMRVK', 1-175 <DUS2>
A/Cross-references: GB:I07127; NID:9349550; PIDN:AAA41805.1; PID:9349551
A/Note: an incorrect initiation codon was used
R/Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dag
orn, J. Physiol. 265, G611-G618, 1993
A/Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is ex
A/Reference number: I51899; MUID:94056762; PMID:8238545
A/Accession: I51899
A/Status: preliminary; translated from GB/DMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-175 <IOV1>
A/Cross-references: GB:98049; NID:9393210; PIDN:AAA16341.1; PID:9393211
A/Note: in Genbank entry RAMPAPC, release 113.0, the source is designated as Rattus r
R/Kamimura, T.; West, C.; Beutler, E.
Gene 118, 299-300, 1992
A/Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A/Reference number: JCI257; MUID:92380521; PMID:1511905
A/Accession: JCI257
A/Molecule type: mRNA
A/Residues: 1-6, 'S', '8-175 <KAM>
A/Cross-references: GB:843715; NID:9254694; PIDN:AAE23103.1; PID:9254695
R/Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A/Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein
A/Reference number: A41719; MUID:92105133; PMID:1722211
A/Accession: A41719
A/Molecule type: mRNA
A/Residues: 1-175 <IOV2>
A/Cross-references: GB:M55149; NID:9206030; PIDN:AAA11807.1; PID:9206031
A/Note: the amino-terminal residue of the mature protein was identified as Glu
C/Genetics:
A/Gene: pap
A/Introns: 26/1; 65/3; 111/3; 154/1
A/Note: the first intron occurs before the initiator codon
C/Superfamily: tetraneurin; C-type lectin homology
C/Keywords: lectin; pancreas
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F.40-171/Domain: C-type lectin homology <LCH>
F.40-51,68-171,146-163/disulfide bonds: #status predicted

Query Match 5.7%; Score 10; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSMMLSLCLM 18
DB 10 MSMMLSLCLM 19

RESULT 2
S29822
pancreatitis-associated protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C/Accession: S29822
R/Itoh, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A/Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homo
A/Reference number: S29821; MUID:93176807; PMID:7679928
A/Accession: S29822
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-175 <ITO>
A/Cross-references: GB:D13509; NID:9286106; PIDN:AAA02727.1; PID:9286107
C/Superfamily: tetraneurin; C-type lectin homology
F.40-171/Domain: C-type lectin homology <LCH>

Query Match 5.7%; Score 10; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0085;

Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	9	MSMMLSCIM	18						
Db	10	MSMMLSCIM	19						

Search completed: April 16, 2003, 10:50:48
Job time : 18 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:47:30 ; Search time 12 seconds

(Without alignments)
601.407 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MLPMTLCRMSWMLSLCLMFL.....QKWRDPENCNELPYICKFKV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	175	1	PBQG_HUMAN
2	10	5.7	174	1	PAP3_MOUSE
3	10	5.7	175	1	PAP1_MOUSE
4	10	5.7	175	1	PAP1_RAT

ALIGNMENTS

RESULT 1
PBQG_HUMAN STANDARD; PRT: 175 AA.
AC 092778; F70109;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatic beta cell growth factor precursor (Islet neogenesis DE associated protein).
GN INGP.
OS Homo sapiens (Human), and
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606, 10036;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS OF 104-118.
RC STRAIN=lake view Golden; TISSUE=Pancreas;
RX MIMLINE=97296198; PubMed=9151782;
RA Rafaele R., Pittenger G.L., Barlow S.W., Qin X.F., Yan B.,
RA Rosenberg L., Duguid W.P., Vink A.I.;
RT "Cloning and sequencing of the pancreatic islet neogenesis associated RT protein (INGAP) gene and its expression in islet neogenesis in hamsters.";

RL 1. Clin. Invest. 99:2100-2109(1992).
CC FUNCTION: CONSTITUENT OF ILIOTROPIN, WHICH IS A PARTIALLY PURIFIED
CC PREPARATION OF CELLOPHANE WRAPPING (CW) PANCREATA. CAPABLE OF
CC INITIATING DUCT CELL PROLIFERATION, A PREREQUISITE FOR ISLET
CC NEOGENESIS.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN CW ANIMALS PANCREAS AND TO A
CC LESSER EXTENT IN DUODENUM. IN PANCREAS IT IS FOUND IN ACINAR
CC CELLS, BUT NOT IN ISLETS.
CC -1- INDUCTION: FOUND 1 AND 2 DAYS AFTER CELLOPHANE WRAPPING, ABSENT BY
CC THE 6TH DAY. THIS PERIOD COINCIDES WITH ISLET NEOGENESIS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-2 OR MET-5 IS THE
CC INITIATOR.
CC
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CC
DR EMBL: U41737; AAB86497.1; ALT_INIT.
DR EMBL: U41738; AAB16754.1; ALT_INIT.
DR HSSP: P05451; 10DD.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; Lectin_c; 1.
DR PRINTS: PR01504; PNCREATITSAP.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SO SEQUENCE 175 AA; 19940 MW; 3854F36A35D17CE CRC64;

Query Match 100.0%; Score 174; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.5e-176;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPMTLCRMSWMLSLCLMFLSMVEGESOKRLPSSRTICPOGSVAAGSYCYSLILPOTW 60
DB 2 MLPMTLCRMSWMLSLCLMFLSMVEGESOKRLPSSRTICPOGSVAAGSYCYSLILPOTW 61
OY 61 SNAELSCQMHSGHIAFLITSTGETTFVSSLVKNSLTAYOTIYIGLHDPHSGTLPNGSGMK 120
DB 62 SNAELSCQMHSGHIAFLITSTGETTFVSSLVKNSLTAYOTIYIGLHDPHSGTLPNGSGMK 121
OY 121 MSSSVLTFYNNERNPSTIADRGCAVLSOKSGQKWRDPENCNELPYICKFKV 174
DB 122 MSSSVLTFYNNERNPSTIADRGCAVLSOKSGQKWRDPENCNELPYICKFKV 175

RESULT 2
PAP3_MOUSE STANDARD; PRT: 174 AA.
AC 009049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 3 precursor (REG III-gamma).
GN PAP3 OR RBG3G.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=Liver, and Pancreas;
RX MEDLINE-97208868; PubMed-9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.,
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RT gene 185:159-168(1997).
CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
CC BACTERIAL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL
CC INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
CC HEALTHY PANCREAS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D63361; BAA18930.1; -
DR EMBL: D63362; BAA18931.1; -
DR HSSP: P05451; ILIT.
DR MGD: MGI:109406; Reg3g.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; lectin_C.1.
DR PRINTS: PRO1504; PNCREATITISAP.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
DR SIGNAL: Lectin; Inflammatory response; Acute phase; Multigene family.
KW SIGNAL; 1 26
FT CHAIN 1 26 PNCREATITIS-ASSOCIATED PROTEIN 3.
FT DOMAIN 27 174 C-TYPE LECTIN (LONG FORM).
FT DISULFID 38 172 BY SIMILARITY.
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 170 BY SIMILARITY.
FT DISULFID 145 162 BY SIMILARITY.
SQ SEQUENCE 174 AA; 19307 MW; 5575E9E564D8CF CRC64;

Query Match 5.7%; Score 10; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLSCIM 18
DB 10 MSWMLSCIM 19

RESULT 3
PAP1_MOUSE STANDARD: PRT; 175 AA.
AC P35230;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
GN PAP1 OR PAP OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-Pancreas, and Small Intestine;
RX MEDLINE-93176807; PubMed-7679928;
RA Itoh T., Teraoka H.;

```

```

RT "Cloning and tissue-specific expression of cDNAs for the human and
RT mouse homologues of rat pancreatitis-associated protein (PAP).";
RT Blochim. Biophys. Acta 1172:184-186(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-Pancreas;
RX MEDLINE-97208868; PubMed-9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.,
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RT gene 185:159-168(1997).
CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
CC BACTERIAL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
CC PANCREATIC ACINAR CELLS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL
CC INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
CC HEALTHY PANCREAS.
CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
CC PANCREATIC INFLAMMATION.
CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
DR EMBL: D13509; BAA02727.1; -
DR EMBL: D63359; BAA18928.1; -
DR EMBL: D63360; BAA18929.1; -
DR PIR: S29822; S29822.
DR HSSP: P05451; ILIT.
DR MGD: MGI:97478; Pap.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; lectin_C.1.
DR PRINTS: PRO1504; PNCREATITISAP.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
DR SIGNAL: Lectin; Inflammatory response; Acute phase; Multigene family.
KW SIGNAL; 1 26
FT CHAIN 1 26 PNCREATITIS-ASSOCIATED PROTEIN 1.
FT DOMAIN 27 175 C-TYPE LECTIN (LONG FORM).
FT DISULFID 38 173 BY SIMILARITY.
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 5.7%; Score 10; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLSCIM 18
DB 10 MSWMLSCIM 19

RESULT 4
PAP1_RAT STANDARD: PRT; 175 AA.
AC P25031; Q64231; Q64102;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (Peptide 23) (REG-2).
GN PAP1 OR PAP OR REG2.

```

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-39.
 RC STRAIN-Sprague-Dawley; TISSUE-Pancreas;
 RX MEDLINE=92105133; PubMed=1722211;
 RA Iovanna J., Orelle B., Keim V., Dagorn J.-C.;
 RT "Messenger RNA sequence and expression of rat pancreatitis-associated
 RT protein, a lectin-related protein overexpressed during acute
 RT experimental pancreatitis.";
 RL J. Biol. Chem. 266:24664-24669(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Intestine;
 RX MEDLINE=94056762; PubMed=8238345;
 RA Iovanna J.L., Keim V., Bosshard A., Orelle B., Frigerio J.M.,
 RA Dusetti N., Dagorn J.C.;
 RT "PAP, a pancreatic secretory protein induced during acute
 RT pancreatitis, is expressed in rat intestine.";
 RL Am. J. Physiol. 265:G611-G618(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; TISSUE-Liver;
 RX MEDLINE=93300847; PubMed=8314803;
 RA Dusetti N.J., Frigerio J.M., Keim V., Dagorn J.C., Iovanna J.;
 RT "Structural organization of the gene encoding the rat pancreatitis-
 RT associated protein. Analysis of its evolutionary history reveals an
 RT ancient divergence from the other carbohydrate-recognition domain-
 RT containing genes.";
 RL J. Biol. Chem. 268:14470-14475(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92380521; PubMed=1511905;
 RA Kamimura T., West C., Beutler E.;
 RT "Sequence of a cDNA clone encoding a rat Reg-2 protein.";
 RL Gene 118:299-300(1992).
 RN [5]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Sprague-Dawley; TISSUE-Pituitary;
 RX MEDLINE=95203187; PubMed=7895644;
 RA Katsumata N., Chakraborty C., Myal Y., Schroeder I.C.,
 RA Murphy L.J., Shu R.P., Friesen H.G.;
 RT "Molecular cloning and expression of peptide 23, a growth hormone-
 RT releasing hormone-inducible pituitary protein.";
 RL Endocrinology 136:1332-1339(1995).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION. SECRETED ALSO BY PITUITARY CELLS; THE
 CC SECRETION THERE IS STIMULATED BY GH-RELEASING HORMONE AND
 CC INHIBITED BY SOMATOSTATIN.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M55149; AAA1807.1; -
 DR EMBL: M98049; AAA16341.1; -
 DR EMBL: L07127; AAA41805.1; ALT_INT.
 DR EMBL: S43715; AAB3103.1; -
 DR EMBL: S77413; AAB3848.2; -
 DR PIR: A41719; A41719.

DR HSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin.C.
 DR InterPro: IPR003900; Pancreatis_ac.
 DR Pfam: PF00059; Lectin_c; 1.
 DR PRINTS: PR01504; PNCREATITISAP.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
 DR PROSITE: PS00615; C-TYPE_LLECTIN_2; 1.
 DR PROSITE: PS50041; C-TYPE_LLECTIN; 1.
 KW Signal; Lectin; Inflammatory response; Acute phase.
 FT SIGNAL 1 26
 FT CHAIN 27 175 PNCREATITIS-ASSOCIATED PROTEIN 1.
 FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 FT CONFLICT 7 7 F -> S (IN REF. 4).
 FT CONFLICT 123 123 S -> T (IN REF. 5).
 SQ SEQUENCE 175 AA; 19617 MW; C43892BP31B0B525 CRC64;
 Query Match 5.78; Score 10; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 9 MSIMILSCLM 18
 DB 10 MSIMILSCLM 19
 Search completed: April 16, 2003, 10:49:46
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:47:51 ; Search time 30 Seconds
(without alignments)
1195.073 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 174
Sequence: 1 MLPMTLCRMSNMLSCMLF.....QKMDPNCENELPYCKFKV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 segs, 206047115 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	40.2	138	11	09QYF7 mesocricetu
2	11	6.3	98	11	09QYF8 mus musculi
3	11	6.3	175	11	09JMH1 mus musculi
4	11	6.3	175	11	09QUS9 mus musculi

ALIGNMENTS

RESULT 1
ID 09QYF7 PRELIMINARY: PRT: 138 AA.
AC 09QYF7:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Islet neogenesis associated protein (Fragment).
GN INGP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nata K., Akiyama T., Shervani N.J., Kobayashi S.,
RA Tomioka-Kumagai T., Ito S., Takasawa S., Okamoto H.,
RT Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region."
RL Gene 246:111-122(2000).
DR EMBL; AB035211; BAA88566.1; -.
DR HSSP; P05451; 10DD.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C_1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_Type_Lectin_1; 1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 15585 MW; 4E3BB8AADA1B524 CRC64;

Query Match 40.2%; Score 70; DB 11; Length 138;
Best local Similarity 100.0%; Pred. No. 8.8e-68;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 TPCPGSVAGSYCYSLILIPQWNAELSCOMPSGHIAFLSTGRTFVSSIVKNSLT 96
DB 1 TPCPGSVAGSYCYSLILIPQWNAELSCOMPSGHIAFLSTGRTFVSSIVKNSLT 60
QY 97 AYOYTWIGLH 106
DB 61 AYOYTWIGLH 70

RESULT 2
ID 09QYF8 PRELIMINARY: PRT: 98 AA.
AC 09QYF8:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Reg III delta (Fragment).
GN INGP OR REG3A OR REG3D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nata K., Akiyama T., Shervani N.J., Kobayashi S.,
RA Tomioka-Kumagai T., Ito S., Takasawa S., Okamoto H.,
RT Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region."
RL Gene 246:111-122(2000).
DR EMBL; AB035203; BAA88562.1; -.
DR HSSP; P05451; 1LIT.
DR MGD; MGI:109408; Reg3a.
DR MGD; MGI:1353426; Ingapr.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C_1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11248 MW; 871BC93FAD00595 CRC64;

Query Match 6.3%; Score 11; DB 11; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 77 FVSSLVKNLSLT 87

RESULT 3

09JMH1 PRELIMINARY; PRT; 175 AA.

AC 09JMH1
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE INGAAP related protein.
GN INGAAP OR INGAAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BDF-1; TISSUE=DIDENDUM;
RX MEDLINE-20033449; PubMed-10564727;
RA Itakura M.;
RA Itakura K., Yamaoka T., Moritani M., Yoshimoto K., Kuroda Y.,
RT "Molecular cloning and tissue-specific expression of a new member of
the regenerating protein family, islet neogenesis-associated protein-
related protein."
RL Blochim. Biophys. Acta 1500:142-146(2000).
DR EMBL; AB028625; BAA92141.1; -
DR HSP; P05451; IQDD.
DR MGD; MGI:1353426; Ingaap.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 175 AA; 20021 MW; 0A92F6112BC6B53 CRC64;

Query Match

Best Local Similarity 6.3%; Score 11; DB 11; Length 175;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 87 FVSSLVKNLSLT 97

RESULT 4

09QUS9 PRELIMINARY; PRT; 175 AA.

AC 09QUS9
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE REG III delta precursor (Islet neogenesis associated protein-related
protein).
GN INGAAP OR REG3D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Abe M., Nata K., Tomioka-Kumagai T., Takawa S., Ito S., Okamoto H.;
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
of all three types of Reg family genes in 75-Kilobase mouse genomic
region."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J; TISSUE-PANCREAS;
RX MEDLINE-21085660; PubMed-11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Futuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustafson S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
DR EMBL; AB035204; BAA8564.1; -
DR EMBL; AB035205; BAA8565.1; -
DR EMBL; AK019033; BAB31518.1; -
DR HSP; P05451; IQDD.
DR MGD; MGI:1353426; Ingaap.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATTISAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 175 AA; 20037 MW; 0A89D67512BC6B53 CRC64;

Query Match

Best Local Similarity 6.3%; Score 11; DB 11; Length 175;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 87 FVSSLVKNLSLT 97

Search completed: April 16, 2003, 10:50:24
Job time : 30 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:48:51 ; Search time 15 Seconds
(without alignments)
341.306 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 174
1 MPMPTLCRMSMLSCMLF.....QKWRDNCENELPYICKFY 174

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 10

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	174	100.0	174	2	US-08-401-530A-2
2	174	100.0	174	2	US-08-709-662-2
3	174	100.0	175	1	US-08-909-725-6
4	25	14.4	26	1	US-08-909-725-5
5	11	6.3	175	2	US-08-401-530A-3
6	11	6.3	175	2	US-08-709-662-3
7	10	5.7	184	1	US-07-778-156-2
8	10	5.7	184	2	US-08-422-166-2

ALIGNMENTS

RESULT 1
US-08-401-530A-2
; Sequence 2, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vink, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-530A-2
Query Match 100.0%; Score 174; DB 2; Length 174;
Best local similarity 100.0%; Pred. No. 3.1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPMPTLCRMSMLSCMLFVSWGEESQKLPSSRTICPGSVAYGSCYSLILPQTW 60
DB 1 MPMPTLCRMSMLSCMLFVSWGEESQKLPSSRTICPGSVAYGSCYSLILPQTW 60
QY 61 SNAELSCQHFSGHAFLLSTGEITFVSSLVKNLSITAYQYIMGLHPHSHGLPNSGWR 120
DB 61 SNAELSCQHFSGHAFLLSTGEITFVSSLVKNLSITAYQYIMGLHPHSHGLPNSGWR 120
QY 121 WSSSNVLTFFNNERNPSTADNGYCAVLSQKSGQKWRDFNCENELPYICKFY 174
DB 121 WSSSNVLTFFNNERNPSTADNGYCAVLSQKSGQKWRDFNCENELPYICKFY 174
RESULT 2
US-08-709-662-2
; Sequence 2, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vink, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570, 59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-662-2

Query Match 100.0%; Score 174; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 3, 1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCRMWMLSCMLFSLWVGEESOKKLPSSRITPCPGSVAYGSCYSLILIPQW 60
DB 1 MLPTLCRMWMLSCMLFSLWVGEESOKKLPSSRITPCPGSVAYGSCYSLILIPQW 60
QY 61 SNAELSCQMHFSGHLAFLSTGEITFVSSLVKNSLTAYQYIWIIGLHDPHSGTLPNGSGWK 120
DB 61 SNAELSCQMHFSGHLAFLSTGEITFVSSLVKNSLTAYQYIWIIGLHDPHSGTLPNGSGWK 120
QY 121 WSSSNVLTFFYNNERPSTADRGYCAVLSOKSGFQKMRDFNCENELPYICKFKV 174
DB 121 WSSSNVLTFFYNNERPSTADRGYCAVLSOKSGFQKMRDFNCENELPYICKFKV 174

RESULT 3
US-08-909-725-6
Sequence 6, Application US/08909725
Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron
APPLICANT: Pittenger, Gary
APPLICANT: Rafaeloff-Phail, Ronlt
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: IN GAP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570, 05173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-909-725-6

Query Match 100.0%; Score 174; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 3, 1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCRMWMLSCMLFSLWVGEESOKKLPSSRITPCPGSVAYGSCYSLILIPQW 60
DB 2 MLPTLCRMWMLSCMLFSLWVGEESOKKLPSSRITPCPGSVAYGSCYSLILIPQW 61
QY 61 SNAELSCQMHFSGHLAFLSTGEITFVSSLVKNSLTAYQYIWIIGLHDPHSGTLPNGSGWK 120
DB 62 SNAELSCQMHFSGHLAFLSTGEITFVSSLVKNSLTAYQYIWIIGLHDPHSGTLPNGSGWK 121
QY 121 WSSSNVLTFFYNNERPSTADRGYCAVLSOKSGFQKMRDFNCENELPYICKFKV 174
DB 122 WSSSNVLTFFYNNERPSTADRGYCAVLSOKSGFQKMRDFNCENELPYICKFKV 175

RESULT 4
US-08-909-725-5
Sequence 5, Application US/08909725
Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron
APPLICANT: Pittenger, Gary
APPLICANT: Rafaeloff-Phail, Ronlt
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: IN GAP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570, 05173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-909-725-5

Query Match 14.4%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.9e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPWTCRMSMMLSCIMPLSWYEG 25
Db 2 MLPWTCRMSMMLSCIMPLSWYEG 26

RESULT 5

US-08-401-530A-3
Sequence 3, Application US/08401530A
Patent No. 5834590

GENERAL INFORMATION:

APPLICANT: Vlnlk, Aaron I.

APPLICANT: Pittenger, Gary L.

APPLICANT: Katseloff, Ronit

APPLICANT: Rosenberg, Lawrence

APPLICANT: Duguid, William P.

TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESS: Banner & Allegretti

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: US

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401,530A

FILING DATE: 22-FEB-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.48743

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Rattus rattus

US-08-401-530A-3

Query Match 6.3%; Score 11; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 YQYIWIGLHDP 108

Db 99 YQYIWIGLHDP 109

RESULT 6

US-08-709-662-3

Sequence 3, Application US/08709662

Patent No. 5840531

GENERAL INFORMATION:

APPLICANT: Vlnlk, Aaron I.

APPLICANT: Pittenger, Gary L.

APPLICANT: Katseloff, Ronit

APPLICANT: Rosenberg, Lawrence

APPLICANT: Duguid, William P.

TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESS: Banner & Witcoff, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: US

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,662

FILING DATE: 09-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.59178

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Rattus rattus

US-08-709-662-3

Query Match 6.3%; Score 11; DB 2; Length 175;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 YQYIWIGLHDP 108

Db 99 YQYIWIGLHDP 109

RESULT 7

US-07-778-156-2

Sequence 2, Application US/07778156

Patent No. 5436169

GENERAL INFORMATION:

APPLICANT: IOVANNA, JUAN-LUCIO

APPLICANT: KEIM, VOLKER

APPLICANT: DAGORN, JEAN-CHARLES

TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE

TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 543616man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELEPHONE: (703)521-4500
TELEFAX: (703)485-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-778-156-2

Query Match 5.7%; Score 10; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

RESULT 8
US-08-422-166-2
Sequence 2, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELEPHONE: (703)521-4500
TELEFAX: (703)485-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-422-166-2

Query Match 5.7%; Score 10; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

Search completed: April 16, 2003, 10:51:09
Job time : 15 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 10:49:31 ; Search time 19 seconds
(Without alignments)
692.464 Million cell updates/sec

Title: US-08-401-530-2
Perfect score: 174
Sequence: 1 MPMTCRSMMLSLCLMT.....QKWRDPCNCELPIYICKFV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PT_NEM_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	12.1	21	US-10-036-418-1	Sequence 1, Appli
2	15	8.6	15	US-10-036-418-2	Sequence 2, Appli
3	14	8.0	14	US-10-036-418-3	Sequence 3, Appli
4	14	8.0	14	US-10-036-418-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-036-418-1
; Sequence 1, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT APPLICATION NUMBER: US/10/036,418

CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Cricetus

Query Match 12.18; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-036-418-1
QY 19 FLSWEGESOKRLPSSRTIC 39
DB 1 FLSWEGESOKRLPSSRTIC 21

RESULT 2
US-10-036-418-2
; Sequence 2, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cricetus

Query Match 8.64; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 IGLHPSHGTLPGNS 117
DB 1 IGLHPSHGTLPGNS 15

RESULT 3
US-10-036-418-3
; Sequence 3, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cricetus

Query Match 8.08; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 IAADRGYCAVLSQK 151
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DB 1 IAADRGYCAVLSQK 14

RESULT 4

US-10-036-418-4
; Sequence 4, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vank, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cricetus
US-10-036-418-4

Query Match 8.0%; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 150 OKSGFOKWRDENCE 163
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DB 1 OKSGFOKWRDENCE 14

Search completed: April 16, 2003, 10:51:34
Job time : 19 secs